

JC05 Rec'd PCT/PTO 25 FEB 2002



00270

PATENT TRADEMARK OFFICE

Attorney's Docket No.: WST89AUSA

TRANSMITTAL LETTER TO THE U.S. ELECTED OFFICE
(EO/US) - ENTRY INTO NATIONAL STAGE UNDER 35 USC 371PCT/US00/23723

International Application No.

30 August 2000

International Filing Date

31 August 1999

Priority Date Claimed

BRIDGING INTEGRATOR-2 (BIN2) NUCLEIC ACID MOLECULES AND
PROTEINS AND USES THEREFOR

Title of Invention

George C. Prendergast and Kai Ge

Applicant(s) for EO/US

Assistant Commissioner for Patents
US Patent and Trademark Office
Box PCT
Washington, DC 20231
Attn: EO/US

Sir:

Applicant herewith submits to the United States Elected Office
(EO/US) the following items under 35 USC 371:

- (1) This express request to immediately begin national examination procedures (35 USC 371(f)).
- (2) A copy of the cover sheet for the published International Application along with a copy of the specification as filed: 65 pages, including 5 pages of claims, 8 sheets of drawings, 9 pages Sequence Listing, and a copy of the 3 page International Search Report.
- (3) a copy of the 5 page Request form.
- (4) a first Preliminary Amendment for entry prior to calculation of the filing fees.
- (5) our check in the amount of \$355.00, covering the basic national fee as set forth in 37 CFR 1.492(a)(1) and based on the first Preliminary Amendment (1 total claims; 1 independent; and no multiple dependent).

Express Mail No. ET033626852US

- (6) a second Preliminary Amendment.
- (7) Our check in the amount of \$90.00, covering the extra claim fees after entry of the second Preliminary Amendment (30 total claims; 3 independent; and no multiple dependent).
- (8) Three (3) pages executed Combined Declaration and Power of Attorney form.
- (9) an Assignee Information Sheet
- (10) A 9 pages Sequence Listing (provided in specification).
- (11) A 3.5" computer-readable diskette.
- (12) A 1 page Statement under 37 CFR §1.821(f) and §1.825(a) and (b).

Copies of the following miscellaneous items are also enclosed:

- (13) Copy of the 3 page Demand for International Preliminary Examination.

Please charge any additional fees which may be required to effect entry into the National Phase and credit any overpayment to Deposit Account No. 08-3040.

Please direct all communications concerning this application to the undersigned.

Respectfully submitted,

HOWSON AND HOWSON
Attorneys for the Applicants

By Mary E. Bak
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PTO/SB/17 (10-01)

Approved for use through 10/31/2002. OMB 0651-0032

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**FEE TRANSMITTAL
for FY 2002**

Patent fees are subject to annual revision.

Complete if Known

Application Number	JC13 REC'd PCT/PTC 25 FEB 2002
Filing Date	02/25/2002
First Named Inventor	George C. Prendergast et al
Examiner Name	
Group Art Unit	
Attorney Docket No.	WST89AUSA

TOTAL AMOUNT OF PAYMENT (\$) 355.00

METHOD OF PAYMENT

- 1.
- ☒
- The Commissioner is hereby authorized to charge indicated fees and credit any overpayments to:

Deposit Account Number 08-3040

Deposit Account Name Howson and Howson

- ☒
- Charge Any Additional Fee Required Under 37 CFR 1.16 and 1.17

- ☒
- Applicant claims small entity status. See 37 CFR 1.27

- 2.
- ☒
- Payment Enclosed:

☒ Check ☐ Credit card ☐ Money Order ☐ Other**FEE CALCULATION****1. BASIC FILING FEE**

Large Entity Small Entity

Fee Code (\$)	Fee Code (\$)	Fee Description	Fee Paid
101 740 201 370	Utility filing fee		355.00
106 330 206 165	Design filing fee		
107 510 207 255	Plant filing fee		
108 740 208 370	Reissue filing fee		
114 160 214 80	Provisional filing fee		

SUBTOTAL (1) (\$) 355.00

2. EXTRA CLAIM FEES

Total Claims	Extra Claims	Fee from below	Fee Paid
1	-20** = 0	9.00	0.00
1	-3** = 0	42.00	0.00
Multiple Dependent		140.00	0.00

Large Entity Small Entity

Fee Code (\$)	Fee Code (\$)	Fee Code (\$)	Fee Description
103 18 203 9	Claims in excess of 20		
102 84 202 42	Independent claims in excess of 3		
104 280 204 140	Multiple dependent claim, if not paid		
109 84 209 42	** Reissue independent claims over original patent		
110 18 210 9	** Reissue claims in excess of 20 and over original patent		

SUBTOTAL (2) (\$) 0.00

**or number previously paid, if greater; For Reissues, see above

FEE CALCULATION (continued)**3. ADDITIONAL FEES**

Large Entity Fee Code (\$)	Small Entity Fee Code (\$)	Fee Description	Fee Paid
105 130 205 65	Surcharge - late filing fee or oath		
127 50 227 25	Surcharge - late provisional filing fee or cover sheet		
139 130 139 130	Non-English specification		
147 2,520 147 2,520	For filing a request for ex parte reexamination		
112 920* 112 920*	Requesting publication of SIR prior to Examiner action		
113 1,840* 113 1,840*	Requesting publication of SIR after Examiner action		
115 110 215 55	Extension for reply within first month		
116 400 216 200	Extension for reply within second month		
117 920 217 460	Extension for reply within third month		
118 1,440 218 720	Extension for reply within fourth month		
128 1,960 228 980	Extension for reply within fifth month		
119 320 219 160	Notice of Appeal		
120 320 220 160	Filing a brief in support of an appeal		
121 280 221 140	Request for oral hearing		
138 1,510 138 1,510	Petition to institute a public use proceeding		
140 110 240 55	Petition to revive - unavoidable		
141 1,280 241 640	Petition to revive - unintentional		
142 1,280 242 640	Utility issue fee (or reissue)		
143 460 243 230	Design issue fee		
144 620 244 310	Plant issue fee		
122 130 122 130	Petitions to the Commissioner		
123 50 123 50	Processing fee under 37 CFR 1.17(g)		
126 180 126 180	Submission of Information Disclosure Stmt		
581 40 581 40	Recording each patent assignment per property (times number of properties)		
146 740 246 370	Filing a submission after final rejection (37 CFR § 1.129(a))		
149 740 249 370	For each additional invention to be examined (37 CFR § 1.129(b))		
179 740 279 370	Request for Continued Examination (RCE)		
169 900 169 900	Request for expedited examination of a design application		

Other fee (specify)

*Reduced by Basic Filing Fee Paid

SUBTOTAL (3) (\$)

SUBMITTED BY

Name (Print/Type) Mary E. Bak, Esquire

Registration No. (Attorney/Agent)

31,215

Complete if applicable

Telephone (215) 540-9200

Signature

Mary E. Bak

Date

2-25-02

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

Burden Hour Statement: This form is estimated to take 0.2 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

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100-9540 10/069540



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WST89AUSA

JC13 Rec'd PCT/PTO 25 FEB 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of) Group Art Unit:
)
George C. Prendergast et al) Examiner:
)
Appln. No.)
)
Filed: Herewith)
)
For: BRIDGING INTEGRATOR-2 (BIN2))
NUCLEIC ACID MOLECULES AND)
PROTEINS AND USES THEREFOR)

Assistant Commissioner for Patents
U. S. Patent and Trademark Office
Box PCT
Washington, DC 20231

**STATEMENT TO SUPPORT FILING AND SUBMISSION
IN ACCORDANCE WITH 37 CFR §1.821 THROUGH §1.825**

Sir:

I hereby state, in accordance with the requirements of 37 CFR §1.821(f) and to the best of my knowledge and belief that the Sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) Sequence Listing, submitted pursuant to 37 CFR §1.821(c) and (e), respectively.

I hereby state that to the best of my knowledge and belief the submission filed in accordance with the requirements of 37 CFR §1.821(g), does not include new matter.

Respectfully submitted,
HOWSON AND HOWSON
Attorneys for the Applicants

By

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Express Mail No. ET033626852US

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JG13 Rec'd PCT/PTO 25 FEB 2002



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PATENT TRADEMARK OFFICE

WST89AUSA

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of) Group Art Unit:
)
George C. Prendergast et al) Examiner:
)
Appln. No.)
)
Filed: Herewith)
)
For: BRIDGING INTEGRATOR-2 (BIN2)) February 25, 2002
NUCLEIC ACID MOLECULES AND)
PROTEINS AND USES THEREFOR)

Assistant Commissioner for Patents
US Patent and Trademark Office
Box PCT
Washington, DC 20231

PRELIMINARY AMENDMENT A

Sir:

Please amend the above-identified patent application as follows.

In the Claims

Cancel claims 2-27 without prejudice.

Express Mail No. ET033626852US

REMARKS

After entry of this preliminary amendment, the pending claim is claim 1 as presented in the published PCT Application No. WO01/16158. Claims 2-27, as published, are canceled. No new matter is introduced by this preliminary amendment.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version With Markings to Show Changes Made".

Applicants respectfully request that this preliminary amendment be entered prior to calculating the filing fees.

The Director of the U. S. Patent and Trademark Office is hereby authorized to charge any deficiency in any fees due with the filing of this paper or credit any overpayment in any fees to Deposit Account No. 08-3040.

Respectfully submitted,

HOWSON AND HOWSON
Attorneys for the Applicants

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Appendix A
Version with Markings to Show Changes Made

In the claims:

Claims 2-27 have been cancelled.



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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of) Group Art Unit:
)
George C. Prendergast et al) Examiner:
)
Appln. No.)
)
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)
For: BRIDGING INTEGRATOR-2 (BIN2)) February 25, 2002
NUCLEIC ACID MOLECULES AND)
PROTEINS AND USES THEREFOR)

Assistant Commissioner for Patents
US Patent and Trademark Office
Box PCT
Washington, DC 20231

PRELIMINARY AMENDMENT B

Sir:

Please amend the above-identified patent application as follows.

In the Specification

Page 1, line 6, before "Field of the Invention", insert the following new paragraph:

-- Cross-Reference to Related Applications

This is a 371 of PCT/US00/23723, filed August 30, 2000, which claims the benefit of the priority of U. S. Patent Application No. 60/151,554, filed August 31, 1999, now abandoned. --

Express Mail No. ET033626852US

Please enter the attached Abstract of the Disclosure on the attached page as new page 45.

In the Claims

Amend claim 1 as follows.

1. (Amended) A Bin2 peptide or protein having the amino acid sequence of SEQ ID NO: 2 or a fragment thereof.

Add new claims 28-56 as follows.

28. The Bin2 peptide or protein according to claim 1 selected from the group consisting of:

(a) a fragment of Bin2 comprising at least 8 amino acids in length, wherein any of said fragments comprising the sequence of amino acids 23 to 35 of SEQ ID NO: 2 comprise at least 14 amino acids in length; and any fragments comprising the sequence of amino acids 138 to 155 of SEQ ID NO: 2 comprise at least 19 amino acids in length;

(b) an analog or homolog of SEQ ID NO: 2;

(c) a fusion protein comprising the amino acid sequence of (a) or (b) and a fusion partner;

(d) a deletion protein comprising the amino acid sequence of SEQ ID NO: 2 with one to twenty amino acids deleted therefrom.

29. The Bin2 peptide or protein according to claim 28, wherein the fragment of Bin2 has the sequence of amino acids 1 to 221 of SEQ ID NO: 2.

30. The Bin2 peptide or protein according to claim 28, wherein the fragment of Bin2 comprises at least the sequence of amino acids 138 to 155 of SEQ ID NO: 2.

31. The Bin2 peptide or protein according to claim 28, wherein the fragment of Bin2 is at least 8 amino acids in length and comprising a sequence of contiguous amino acids selected from within the sequence of amino acids 1 to 13 of SEQ ID NO: 2.

32. The Bin2 peptide or protein according to claim 28, wherein the fusion partner is selected from the group consisting of glutathione-S-transferase, β -galactosidase, poly-histidine and maltose binding protein.

33. A Bin2 nucleic acid sequence encoding a protein according to claim 1 or a fragment thereof.

34. A nucleic acid sequence selected from the group consisting of:

- (a) a nucleic acid sequence which hybridizes to the sequence of claim 1 under stringent conditions;
- (b) a nucleic acid sequence complementary to the sequence of claim 1; and
- (c) an allelic variant of any of (a) through (b).

35. A nucleic acid sequence encoding a fusion protein comprising the peptide or protein according to claim 28.

36. A vector comprising a nucleic acid sequence according to claim 33 under the control of regulatory sequences which direct expression of the Bin2 protein or fragment.

37. A vector comprising a nucleic acid sequence according to claim 34 said sequence under the control of regulatory sequences.

38. A vector comprising a nucleic acid sequence according to claim 35 said sequence under the control of regulatory sequences.

39. A host cell transformed with a vector according to claim 36.

40. A diagnostic reagent comprising a nucleic acid sequence of claim 33 and a detectable label which is associated with said sequence.

41. A method for diagnosing hepatocarcinoma, said method comprising the steps of amplifying the DNA in a sample from a patient suspected of having hepatocarcinoma using a nucleic acid sequence according to claim 33.

42. A diagnostic reagent comprising a protein according to claim 1 and a detectable label which is associated with said protein.

43. A method for specifically diagnosing cancers associated with inappropriate expression of Bin1 comprising the steps of:

contacting a sample from a human or animal to be diagnosed with the Bin2 protein of claim 1, whereby in the presence of Bin1 in the sample, a complex is formed between Bin1 and the Bin2 protein or reagent, and
analyzing for the presence or quantity of said complex.

44. A method for specifically diagnosing cancers associated with inappropriate expression of Bin1 comprising the steps of:

contacting a sample from a human or animal to be diagnosed with the diagnostic reagent of claim 40, whereby in the presence of Bin1 in the sample, a complex is formed between Bin1 and the Bin2 protein or reagent, and
analyzing for the presence or quantity of said complex.

45. An isolated anti-Bin2 antibody which is specific for the protein of claim 1.

46. The anti-Bin2 antibody according to claim 45, isolated by immunizing said host with the protein of claim 1.

47. The anti-Bin2 antibody according to claim 45 which is selected from the group consisting of a chimeric antibody, a humanized antibody, a monoclonal antibody and a polyclonal antibody.

48. A diagnostic reagent comprising the anti-Bin2 antibody according to claim 47 and a detectable label.

49. A method of diagnosing cancer or hyperplastic disease characterized by inappropriate levels of functional Bin1 levels in a human or an animal, said method comprising the steps of:

contacting a Bin2 protein according to claim 1 with a sample from a human or animal to be diagnosed, whereby in the presence of Bin1, a detectable complex is formed with the Bin2 protein;

analyzing for the presence or absence of said complex; and
comparing the level of complex to a standard, wherein the absence of said detectable label indicates the absence of or decreased levels of functional Bin1.

50. A method of diagnosing cancer or hyperplastic disease characterized by inappropriate levels of functional Bin1 levels in a human or an animal, said method comprising the steps of:

contacting a diagnostic reagent according to claim 48 with a sample from a human or animal to be diagnosed, whereby in the presence of Bin1, a detectable complex is formed with the diagnostic reagent;

analyzing for the presence or absence of said complex; and
comparing the level of complex to a standard, wherein the
absence of said detectable label indicates the absence of or decreased levels of
functional Bin1.

51. A kit for diagnosing a condition associated with Bin2
comprising a diagnostic reagent according to claim 48.

52. A composition comprising an effective amount of a Bin2 protein
of claim 1 and a pharmaceutically acceptable carrier.

53. A method of detecting inappropriate expression of Box-
dependent myc-interacting protein-2 (Bin2) in a patient comprising providing a sample
from a patient suspected of having said inappropriate expression; incubating said
sample in the presence of a diagnostic reagent according to claim 48; and comparing
levels of expression to a normal Bin2 control.

54. A method of detecting inappropriate expression of Box-
dependent myc-interacting peptide-2 (Bin2) in a patient comprising providing a sample
from a patient suspected of having said overexpression and performing nucleic acid
amplification using the nucleic acid sequence according to claim 33.

55. A method of identifying compounds which specifically bind to
Bin2, comprising the steps of contacting said Bin2 or a fragment thereof with a test
compound to permit binding of the test compound to Bin2; and determining the
amount of test compound which is bound to Bin2.

56. A method of identifying compounds which inhibit the binding of Bin2, comprising the steps of:

(a) contacting an amount of immobilized first Bin peptide or a fragment thereof with a test compound and an amount of labeled second Bin peptide or fragment, wherein said first Bin peptide is either a Bin1 or a Bin2 peptide, and the second Bin peptide is the Bin peptide that binds said first Bin peptide;

(b) separating unbound material from immobilized material of (a); and

(c) measuring the amount of label on said immobilized material;

wherein a decrease in the amount of label immobilized in the presence of test compound compared to the amount of label immobilized in the presence of a control peptide or protein, indicates that said test compound inhibits the binding of Bin1 to Bin2.

REMARKS

Upon entry of this second preliminary amendment, claims 1 and 28-56 are in this application. New claims 28-56 are supported throughout the specification and by original claims 2-26, now cancelled. These amendments have eliminated multiple dependencies. No new matter is added by this preliminary amendment.

The attached Abstract of the Disclosure is supported throughout the specification.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. Subject matter being added to the specified sections of the specification is represented by highlighting, while material being deleted is represented by strikeout. The attached Appendix A is captioned "Version With Markings to Show Changes Made".

Attached hereto is a clean copy of all of the pending claims. The attached Appendix B is captioned "Clean Copy of Pending Claims Without Markings".

Applicants respectfully request consideration of the pending claims.

The Director of the U. S. Patent and Trademark Office is hereby authorized to charge any deficiency in any fees due with the filing of this paper or credit any overpayment in any fees to our Deposit Account No. 08-3040.

Respectfully submitted,
HOWSON AND HOWSON
Attorneys for the Applicants

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Appendix A
Version with Markings to Show Changes Made

In the specification:

Page 1, line 6, before "Field of the Invention", insert the following new paragraph:

Cross-Reference to Related Applications

This is a 371 of PCT/US00/23723, filed August 30, 2000, which claims the benefit of the priority of U. S. Patent Application No. 60/151,554, filed August 31, 1999, now abandoned.

In the claims:

Claim 1 has been amended as follows:

1. A Bin2 peptide or protein having the amino acid sequence of SEQ ID NO: 2 or a fragment thereof.

Appendix B
Clean Copy of Pending Claims Without Markings

1. A Bin2 protein having the amino acid sequence of SEQ ID NO: 2 or a fragment thereof.
28. The Bin2 peptide or protein according to claim 1 selected from the group consisting of:
 - (a) a fragment of Bin2 comprising at least 8 amino acids in length, wherein any of said fragments comprising the sequence of amino acids 23 to 35 of SEQ ID NO: 2 comprise at least 14 amino acids in length; and any fragments comprising the sequence of amino acids 138 to 155 of SEQ ID NO: 2 comprise at least 19 amino acids in length;
 - (b) an analog or homolog of SEQ ID NO: 2;
 - (c) a fusion protein comprising the amino acid sequence of (a) or (b) and a fusion partner;
 - (d) a deletion protein comprising the amino acid sequence of SEQ ID NO: 2 with one to twenty amino acids deleted therefrom.
29. The Bin2 peptide or protein according to claim 28, wherein the fragment of Bin2 has the sequence of amino acids 1 to 221 of SEQ ID NO: 2.
30. The Bin2 peptide or protein according to claim 28, wherein the fragment of Bin2 comprises at least the sequence of amino acids 138 to 155 of SEQ ID NO: 2.
31. The Bin2 peptide or protein according to claim 28, wherein the fragment of Bin2 is at least 8 amino acids in length and comprising a sequence of contiguous amino acids selected from within the sequence of amino acids 1 to 13 of SEQ ID NO: 2.

32. The Bin2 peptide or protein according to claim 28, wherein the fusion partner is selected from the group consisting of glutathione-S-transferase, β -galactosidase, poly-histidine and maltose binding protein.

33. A Bin2 nucleic acid sequence encoding a protein according to claim 1 or a fragment thereof.

34. A nucleic acid sequence selected from the group consisting of:

- (a) a nucleic acid sequence which hybridizes to the sequence of claim 1 under stringent conditions;
- (b) a nucleic acid sequence complementary to the sequence of claim 1; and
- (c) an allelic variant of any of (a) through (b).

35. A nucleic acid sequence encoding a fusion protein comprising the peptide or protein according to claim 28.

36. A vector comprising a nucleic acid sequence according to claim 33 under the control of regulatory sequences which direct expression of the Bin2 protein or fragment.

37. A vector comprising a nucleic acid sequence according to claim 34 said sequence under the control of regulatory sequences.

38. A vector comprising a nucleic acid sequence according to claim 35 said sequence under the control of regulatory sequences.

39. A host cell transformed with a vector according to claim 36.

40. A diagnostic reagent comprising a nucleic acid sequence of claim 33 and a detectable label which is associated with said sequence.

41. A method for diagnosing hepatocarcinoma, said method comprising the steps of amplifying the DNA in a sample from a patient suspected of having hepatocarcinoma using a nucleic acid sequence according to claim 33.

42. A diagnostic reagent comprising a protein according to claim 1 and a detectable label which is associated with said protein.

43. A method for specifically diagnosing cancers associated with inappropriate expression of Bin1 comprising the steps of:

contacting a sample from a human or animal to be diagnosed with the Bin2 protein of claim 1, whereby in the presence of Bin1 in the sample, a complex is formed between Bin1 and the Bin2 protein or reagent, and
analyzing for the presence or quantity of said complex.

44. A method for specifically diagnosing cancers associated with inappropriate expression of Bin1 comprising the steps of:

contacting a sample from a human or animal to be diagnosed with the diagnostic reagent of claim 40, whereby in the presence of Bin1 in the sample, a complex is formed between Bin1 and the Bin2 protein or reagent, and
analyzing for the presence or quantity of said complex.

45. An isolated anti-Bin2 antibody which is specific for the protein of claim 1.

46. The anti-Bin2 antibody according to claim 45, isolated by immunizing said host with the protein of claim 1.

47. The anti-Bin2 antibody according to claim 45 which is selected from the group consisting of a chimeric antibody, a humanized antibody, a monoclonal antibody and a polyclonal antibody.

48. A diagnostic reagent comprising the anti-Bin2 antibody according to claim 47 and a detectable label.

49. A method of diagnosing cancer or hyperplastic disease characterized by inappropriate levels of functional Bin1 levels in a human or an animal, said method comprising the steps of:

contacting a Bin2 protein according to claim 1 with a sample from a human or animal to be diagnosed, whereby in the presence of Bin1, a detectable complex is formed with the Bin2 protein;

analyzing for the presence or absence of said complex; and

comparing the level of complex to a standard, wherein the absence of said detectable label indicates the absence of or decreased levels of functional Bin1.

50. A method of diagnosing cancer or hyperplastic disease characterized by inappropriate levels of functional Bin1 levels in a human or an animal, said method comprising the steps of:

contacting a diagnostic reagent according to claim 48 with a sample from a human or animal to be diagnosed, whereby in the presence of Bin1, a detectable complex is formed with the diagnostic reagent;

analyzing for the presence or absence of said complex; and

comparing the level of complex to a standard, wherein the absence of said detectable label indicates the absence of or decreased levels of functional Bin1.

51. A kit for diagnosing a condition associated with Bin2 comprising a diagnostic reagent according to claim 48.

52. A composition comprising an effective amount of a Bin2 protein of claim 1 and a pharmaceutically acceptable carrier.

53. A method of detecting inappropriate expression of Box-dependent myc-interacting protein-2 (Bin2) in a patient comprising providing a sample from a patient suspected of having said inappropriate expression; incubating said sample in the presence of a diagnostic reagent according to claim 48; and comparing levels of expression to a normal Bin2 control.

54. A method of detecting inappropriate expression of Box-dependent myc-interacting peptide-2 (Bin2) in a patient comprising providing a sample from a patient suspected of having said overexpression and performing nucleic acid amplification using the nucleic acid sequence according to claim 33.

55. A method of identifying compounds which specifically bind to Bin2, comprising the steps of contacting said Bin2 or a fragment thereof with a test compound to permit binding of the test compound to Bin2; and determining the amount of test compound which is bound to Bin2.

56. A method of identifying compounds which inhibit the binding of Bin2, comprising the steps of:

- (a) contacting an amount of immobilized first Bin peptide or a fragment thereof with a test compound and an amount of labeled second Bin peptide or fragment, wherein said first Bin peptide is either a Bin1 or a Bin2 peptide, and the second Bin peptide is the Bin peptide that binds said first Bin peptide;
- (b) separating unbound material from immobilized material of (a); and

(c) measuring the amount of label on said immobilized material;

wherein a decrease in the amount of label immobilized in the presence of test compound compared to the amount of label immobilized in the presence of a control peptide or protein, indicates that said test compound inhibits the binding of Bin1 to Bin2.

2/1/12

BRIDGING INTEGRATOR-2 (BIN2) NUCLEIC ACID MOLECULES AND PROTEINS AND USES THEREFOR

This work was supported in part by Grant Nos. DAMD17-96-1-6324 and DAMD 17-98-1-8508 from the US Army Breast and Prostate Cancer Research

5 Programs. The US government has certain rights in this invention.

Field of the Invention

This invention relates generally to cancer diagnosis and therapy, and more specifically, to cancers associated with over- or underexpression of Bin1 or other members of the BAR family of adaptor proteins.

10 Background of the Invention

Bin1/Amphiphysin/RVS (BAR) proteins are a family of adaptor proteins implicated in a diverse set of cellular processes, including tumorigenesis, cell survival, differentiation, and nerve synaptic activity. BAR proteins share a common N-terminal BAR domain also termed the RVS domain. While BAR proteins share a
15 common domain (BAR), they appear to have divergent physiological functions. As one example, amphiphysin is a neuronal protein of this family which is implicated in synaptic vesicle endocytosis [Wigge and McMahon, *Trends Neurosci.* **21**: 339-344 (1998)]. Amphiphysin is also a paraneoplastic autoimmune antigen in cancers of the breast, lung, and other tissues [Antoine *et al.*, *Arch. Neurol.* **56**: 172-177 (1999);
20 Dropcho, *Ann. Neurol.* **39**: 659-667 (1996); Folli *et al.*, *N. Engl. J. Med.* **328**: 546-51 (1993)].

Bin1 (Bridging Integrator-1) is a second, ubiquitous BAR protein that was initially identified in mammalian cells through its ability to interact with and inhibit the oncogenic properties of c-Myc [Sakamuro *et al.*, *Nature Genet.* **14**: 69-77
25 (1996)]. Ubiquitous Bin1 isoforms that localize to the nucleus have tumor suppressor properties and have been implicated in growth control, differentiation, and programmed cell death [Mao *et al.*, *Genomics* **56**: 51-58 (1999); Prendergast,

Oncogene 18: 2966-2986 (1999); Sakamuro *et al.* 1996, cited above; Wechsler-Reya *et al.*, *Mol. Cell. Biol.* 18: 566-575 (1998)].

Other members of the BAR family include the yeast proteins RVS167 and RVS161, which are believed to have some negative role in cell growth regulation.

- 5 There exists a need in the art for compositions and methods useful for diagnosis and treatment of conditions characterized by inappropriate cell growth control, or disorders affecting cell survival, differentiation, endocytosis, and actin organization.

Summary of the Invention

The present invention provides a novel member of the Bin1/
10 Amphiphysin/RVS (BAR) proteins, termed herein Bin2. Bin2 proteins, nucleic acids, and other Bin2 compositions of the invention have a variety of uses relating to regulation of cell growth control, cell survival, differentiation, endocytosis and actin organization, as well for diagnosis and treatment of conditions associated with aberrant cell behavior.

- 15 In one aspect, the present invention provides a Bin2 protein. In one desirable embodiment, the protein has the 564 amino acid sequence of SEQ ID NO:2. In another embodiment, the present invention provides a Bin2 peptide or protein selected from the group consisting of a fragment of Bin2 comprising at least 8 amino acids in length. In one embodiment a fragment of this invention is at least 8
20 contiguous amino acids in length and is selected from amino acids 1 to 13 of SEQ ID NO:2. In another embodiment, a fragment of this invention is at least 14 amino acids in length and includes amino acids 23 to 35 of SEQ ID NO:2, and preferably amino acids 23-45 of SEQ ID NO: 2. In still another embodiment, a fragment includes amino acids 138 - 155 of SEQ ID NO:2 and comprises at least 19 amino acids in
25 length. In still another embodiment, a fragment includes amino acids 179-336, or a smaller fragment of at least 8 amino acids contained therein. Still other fragments may be selected from the sequence. In yet another embodiment, the invention provides analogs or homologs of SEQ ID NO:2. In still another embodiment, the invention provides a fusion protein comprising the amino acid sequence of SEQ ID

NO: 2, a fragment, analog or homolog thereof, and a fusion partner. In still a further embodiment, the invention provides a deletion protein comprising the amino acid sequence of SEQ ID NO:2 with one to twenty amino acids deleted therefrom.

In another aspect, the present invention provides a Bin2 nucleic acid
5 sequence. Desirably, the Bin2 nucleic acid sequence encodes a protein or fragment of the invention (such as those mentioned above) and contains SEQ ID NO:1 or a fragment thereof. In one embodiment, the Bin2 nucleic acid sequence hybridizes to the sequence of SEQ ID NO:1 under stringent conditions. In another embodiment, the invention provides a nucleic acid sequence complementary to the nucleic acid
10 sequence of SEQ ID NO:1. In still another embodiment, the invention provides a nucleic acid sequence encoding a fusion protein of the invention. In a further embodiment, the invention provides an allelic variant of any of the Bin2 nucleic acid sequences of the invention. In still another embodiment, the nucleic acid sequence is an antisense sequence to the sequences described above.

15 In a further aspect, the invention provides a vector comprising a Bin2 nucleic acid sequence of the invention under the control of regulatory sequences which direct expression of the Bin2 protein.

In still another aspect, the invention provides a host cell transformed with the vector of the invention.

20 In yet a further aspect, the invention provides a diagnostic reagent comprising a Bin2 nucleic acid sequence of the invention and a detectable label which is associated with said sequence. Methods of diagnosing conditions associated with inappropriate functional levels, the loss of expression of Bin2 or altered expression of Bin2, e.g., cancers, which use this reagent are also provided.

25 In still a further aspect, the invention provides a diagnostic reagent comprising a Bin2 protein or peptide of the invention and a detectable label which is associated with that protein. Also provided are methods of using this reagent and/or the Bin2 protein for diagnosing cancers associated with inappropriate expression (e.g., overexpression or underexpression or altered expression) of Bin1, to which
30 Bin2 binds. This method involves the steps of contacting a sample from a human or

animal to be diagnosed with the Bin2 protein of the invention, or the diagnostic reagent containing this protein, whereby in the presence of Bin1 in the sample, a complex is formed between Bin1 and the Bin2 protein or reagent, and analyzing for the presence of said complex.

5 In yet another aspect, the invention provides an isolated anti-Bin2 antibody which is specific for the Bin2 protein of the invention.

 In still another aspect, the invention provides a diagnostic reagent comprising the anti-Bin2 antibody of the invention and a detectable label. Further provided by the invention is a method of diagnosing cancer or hyperplastic disease characterized
10 by inappropriate levels or altered expression of functional Bin2 in a human or an animal using the anti-Bin2 antibody or diagnostic reagent of the invention. This method involves contacting an anti-Bin2 antibody or a diagnostic reagent containing same with a sample from a human or animal to be diagnosed, whereby in the presence of Bin2, a detectable complex is formed with the Bin2 protein or diagnostic
15 reagent, analyzing for the presence or absence of said complex; and comparing the level of complex to a standard, wherein the absence of said detectable label indicates the absence of functional Bin2.

 In still another aspect, the invention provides a kit for diagnosing a condition associated with Bin2 comprising a diagnostic reagent of the invention.

20 In a further aspect, the invention provides an anti-idiotypic antibody specific for the anti-Bin2 antibody of the invention.

 In yet another aspect, the invention provides a composition comprising an effective amount of a Bin2 protein or anti-idiotypic of the invention and a pharmaceutically acceptable carrier.

25 In still another aspect, the invention provides a method of detecting inappropriate expression of Box-dependent myc-interacting protein-2 (Bin2) in a patient comprising providing a sample from a patient suspected of having said inappropriate (over- or under-expression) or altered expression; incubating said sample in the presence of an anti-Bin2 antibody or a diagnostic reagent containing
30 same; and comparing levels of expression to a normal Bin2 control.

5 In a further aspect, the invention provides a method of detecting inappropriate expression of Box-dependent myc-interacting peptide-2 (Bin 2) in a patient comprising providing a sample from a patient suspected of having said inappropriate expression and performing nucleic acid amplification using a Bin2 nucleic acid sequence of the invention.

10 In still a further aspect, the invention provides a method of identifying compounds which specifically bind to Bin2 or which specifically inhibit or block the binding of Bin2 to its ligand. In one embodiment, the method involves comprising the steps of contacting said Bin2 or a fragment thereof with a test compound to permit
15 binding of the test compound to Bin2; and determining the amount of test compound which is bound to Bin2. In another embodiment, the invention provides a method of contacting an amount of immobilized first Bin peptide or a fragment thereof with a test compound and an amount of labeled second Bin peptide or fragment, wherein said first Bin peptide is either a Bin1 or a Bin2 peptide, and the second Bin peptide is
20 the Bin peptide that binds said first Bin peptide. Unbound material is separated from immobilized material and the amount of label on said immobilized material is measured. A decrease in the amount of label immobilized in the presence of test compound compared to the amount of label immobilized in the presence of a control peptide or protein, indicates that said test compound inhibits the binding of Bin1 to Bin 2, or vice versa. The invention further provides a compound identified by this method.

Other aspects and advantages of the present invention are described further in the following detailed description of the preferred embodiments thereof.

Brief Description of the Drawings

25 Figs. 1A-1C illustrate the continuous sequence of full-length Bin2 cDNA [SEQ ID NO: 1] and the continuous amino acid sequence encoded thereby [SEQ ID NO: 2]. The initiating methionine codon is underlined and the stop codon TCT is indicated by an asterisk 5' and 3' noncoding sequences are shown.

Fig. 2 provides an alignment of the BAR domains of Bin2 [SEQ ID NO: 2] and Bin1 [SEQ ID NO: 3].

Fig. 3 is an illustration comparing Bin2 structure with other BAR family members.

5 Fig. 4A provides the amino acid sequence alignment of Bin1 [SEQ ID NO: 3], Bin2 [SEQ ID NO: 2], and Daxx [SEQ ID NO: 4].

Fig. 4B is an illustration of the domains in Bin1, Bin2, and Daxx and the relative region of similarity between Bin2 and Daxx (dark shaded).

Fig. 5A is a bar graph illustrating the results of a colony formation assay.
10 HepG2 and A549 cells were transfected with expression vectors and stable transformants were selected by culturing cells in G418. Colonies were scored by methanol fixation and crystal violet staining 2-3 weeks later. The data represent the mean and standard error from three trials.

Fig. 5B is a bar graph that illustrates that Bin2 does not affect the tumor
15 suppressor activity of Bin1. The colony formation assay was performed as above using 10 μ g vector, 5 μ g vector + 5 μ g Bin1 plasmid, or 5 μ g Bin1 + 5 μ g Bin2 plasmids.

Detailed Description of the Invention

The present invention provides novel, isolated mammalian Bin2 nucleic acid
20 sequences, fragments thereof and proteins and peptides encoded thereby. The invention further provides methods of using these sequences, proteins, and compositions containing them for diagnosis and treatment of disorders associated with deregulation, deficiency or amplification of the *c-myc* oncogenes. The present invention further provides methods of using these sequences to generate antibodies
25 and new compositions useful for such diagnosis and treatments.

The present invention provides Bin2 (Bridging INtegrator-2), which is a novel member of the BAR family. Bin2 is expressed predominantly in hematopoietic cells and can form a stable complex with Bin1. Bin2 is upregulated during differentiation of granulocytes, thereby functioning in that cell lineage. Bin2 lacks sequences found

in Bin1 that mediate c-Myc interaction. Bin2 also lacks sequences found in amphiphysin that mediate interaction with endocytotic machinery in the brain. In addition, Bin2 lacks a C-terminal region SH3 domain, instead including a C-terminal extension that is unrelated to other members of the BAR family. Database comparisons with Bin2 revealed a previously unrecognized region of similarity between BAR family proteins and Daxx, a nucleocytoplasmic adaptor implicated in programmed cell death, JNK signaling, and chromosomal regulation [Chang *et al.*, *Science* **281**: 1860-1863 (1998); Pluta *et al.*, *J. Cell Sci.* **111**: 2029-2041 (1998); Yang *et al.*, *Cell* **89**: 1067-1076 (1997)], within the central part of these proteins.

10 The human Bin2 gene was mapped to chromosome 4q22.1, within a region that is frequently deleted in breast and liver cancers. However, unlike Bin1, which is ubiquitous and growth inhibitory, Bin2 was expressed predominantly in hemapoietic cells and was found to lack detectable antiproliferative activity. Thus, Bin2 is a novel BAR protein which has nonredundant functions relative to other members of the

15 BAR family.

Compositions containing Bin2 proteins and nucleic acid sequences are useful for a variety of purposes. These aspects of the invention are discussed in more detail below.

I. Nucleic Acid Sequences

20 The present invention provides mammalian nucleic acid sequences encoding a Bin2 protein or peptide. The nucleic acid sequences of this invention may be isolated from cellular materials with which they are naturally associated or produced using techniques known in the art. In one embodiment, the present invention provides Bin2 nucleic acid sequence SEQ ID NO:1 and fragments of at least eight contiguous amino

25 acids thereof. However, the present invention is not limited to these nucleic acid sequences.

Given the sequences of the Bin2 DNA [SEQ ID NO: 1], one of skill in the art can readily obtain the corresponding anti-sense strands to these sequences. Further,

using known techniques, one of skill in the art can readily obtain further sequences, including cDNA sequences or the corresponding RNA sequences, as desired.

Allelic variants of these sequences within a species (i.e., sequences containing some individual nucleotide differences from a more commonly occurring sequence
5 within a species, but which nevertheless encode the same protein or a protein with the same function) may also be readily obtained given the knowledge of the nucleic acid sequence provided by this invention.

The present invention further encompasses nucleic acid sequences capable of hybridizing under stringent conditions [see, J. Sambrook et al, Molecular Cloning: A
10 Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory (1989)] to the sequences of the invention, SEQ ID NO: 1, their anti-sense strands, or biologically active fragments thereof. An example of a highly stringent hybridization condition is hybridization at 2XSSC at 65°C, followed by a washing in 0.1XSSC at 65°C for an hour. Alternatively, an exemplary highly stringent hybridization condition is in 50%
15 formamide, 4XSSC at 42°C. Moderately high stringency conditions may also prove useful, e.g. hybridization in 4XSSC at 55°C, followed by washing in 0.1XSSC at 37°C for an hour. An alternative exemplary moderately high stringency hybridization condition is in 50% formamide, 4XSSC at 30°C.

According to the invention, the nucleic acid sequences may be modified.
20 Utilizing the sequence data provided herein, it is within the skill of the art to obtain or prepare synthetically or recombinantly other polynucleotide sequences, or modified polynucleotide sequences, encoding the full-length proteins or useful fragments of the invention. Such modifications at the nucleic acid level include, for example, modifications to the nucleotide sequences which are silent or which change the amino
25 acids, e.g. to improve expression or secretion. Also included are allelic variations, caused by the natural degeneracy of the genetic code.

Also encompassed by the present invention are nucleotide sequences encoding mutants of the Bin2 peptides and proteins provided herein. Such mutants include amino terminal, carboxy terminal or internal deletions, which substantially
30 retain the biological activity (e.g., the antigenicity and/or the ability to bind Bin1) of

the full-length Bin2 or other proteins or fragments. Such a truncated, or deletion mutant may be expressed for the purpose of affecting the activity of the full-length or wild-type gene or gene fragments.

Thus, the invention provides nucleic acid sequence fragments that encode a
5 desirable fragment of Bin2, e.g., a Bin1 binding region. Generally, these
oligonucleotide fragments are at least 15 nucleotides in length. However,
oligonucleotide fragments of varying sizes may be selected as desired. Such
fragments may be used for such purposes as performing polymerase chain reaction
(PCR), e.g., on a biopsied tissue sample.

10 For example, suitable nucleic acid fragments include those encoding the
complete BAR motif or domain (amino acid 1 to 221 or amino acid 1 to 249 of SEQ
ID NO:2) and the putative BAR effector region (amino acid 138 - 155 of SEQ ID
NO:2). In one embodiment a fragment of this invention encodes at least 8 contiguous
amino acids in length, e.g., a fragment selected from amino acids 1 to 13 of SEQ ID
15 NO:2. In another embodiment, a nucleic acid sequence of this invention encodes at
least 14 amino acids in length. Exemplary fragments include those encoding amino
acids 23 to 35 or a peptide within amino acids 23 to 45 of SEQ ID NO:2. In still
another embodiment, a nucleic acid sequence encodes a BIN2 fragment within amino
acids 138 - 155 of SEQ ID NO:2 and comprises at least 19 amino acids in length.
20 Still another nucleic acid sequence of the invention encodes a peptide of at least 8
amino acids in length within amino acids 179 to 336 of SEQ ID NO: 2. Still another
nucleic acid sequence of the invention encodes a peptide of at least 8 amino acids in
length within amino acids 250 to 564 of SEQ ID NO: 2, which is the region unrelated
to the other BAR family proteins. In yet another embodiment, the nucleotide
25 sequences of the invention encode analogs or homologs of SEQ ID NO:2. In still
another embodiment, the nucleotide sequences of this invention encode fusion
proteins comprising the amino acid sequence of SEQ ID NO: 2, a fragment, analog or
homolog thereof, and a fusion partner. In still a further embodiment, a nucleotide
sequence of this invention encodes a deletion protein comprising the amino acid
30 sequence of SEQ ID NO:2 with one to twenty amino acids deleted therefrom. Other

useful fragments may be readily identified by one of skill in the art by resort to conventional techniques.

The nucleotide sequences of the invention may be isolated by conventional uses of polymerase chain reaction or cloning techniques such as those described in
5 obtaining the murine and human sequences, described below. Alternatively, these sequences may be constructed using conventional genetic engineering or chemical synthesis techniques.

These nucleic acid sequences are useful for a variety of diagnostic, prophylactic and therapeutic uses. Advantageously, the nucleic acid sequences are
10 useful in the development of diagnostic probes and antisense probes for use in the detection and diagnosis of cancers and other conditions associated with inappropriate levels of functional Bin2 (and/or its binding partner, Bin1) or altered expression of Bin2 by utilizing a variety of known nucleic acid assays, e.g., Northern and Southern blots, polymerase chain reaction (PCR), and other assay techniques known to one of
15 skill in the art. When used in diagnostic applications, the nucleic acid sequences of the invention may optionally be associated with a detectable label, such as are described in detail below. The nucleic acid sequences of this invention are also useful in the production of the peptides and proteins of the invention *in vitro*, *in vivo*, and *ex vivo*.

20 II. Protein Sequences

The present invention also provides mammalian Bin2 polypeptides or proteins. For convenience throughout this specification, reference will be made to
"Bin2 peptides and proteins", but it will be understood that this term encompasses the fragments, analogs, modified peptides and proteins, fusion proteins, and other amino
25 acid constructs of the invention, except where otherwise specified.

These Bin2 peptides and proteins may be isolated in a form substantially free from other proteinaceous and non-proteinaceous cellular materials (e.g., hepatocytes) or from cell extracts. For example, these peptides and proteins may be isolated from the cellular materials and optionally, further purified using any of a variety of

conventional methods including: liquid chromatography such as normal or reversed phase, using HPLC, FPLC and the like; affinity chromatography (such as with inorganic ligands or monoclonal antibodies); size exclusion chromatography; immobilized metal chelate chromatography; gel electrophoresis; and the like. One of skill in the art may select the most appropriate isolation and purification techniques without departing from the scope of this invention.

Alternatively, the Bin2 peptides and proteins of the invention, described below, may be produced recombinantly following conventional genetic engineering techniques [see e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY and the detailed description of making the proteins below]. In still another alternative, the peptides and proteins of the invention may be produced using conventional chemical synthesis techniques, such as those described in G. Barony and R.B. Merrifield, *The Peptides: Analysis, Synthesis & Biology*, Academic Press, pp. 3-285 (1980), among others. The term "artificial" is used herein to denote the preparation of the construct (e.g., a peptide, protein, nucleic acid, or antibody of the invention) by chemical synthesis, recombinant technology, or other similar means.

The present invention further provides analogs, fragments, and mutant peptides, as well as proteins containing Bin2, or such analogs, fragments or mutants, as described below.

A. Analogs and Modified Peptide and Protein Antigens

Analog or modified versions of the Bin2 proteins and peptides are provided. Typically, analogs differ from the specifically identified proteins by only one to four codon changes. Examples include polypeptides with minor amino acid variations from the illustrated amino acid sequence of Bin2 having conservative amino acid replacements. Conservative replacements are those that take place within a family of amino acids that are related in their side chains and chemical properties. Also provided are homologs of the proteins of the invention which are characterized by having at least 90% identity, and more preferably 95-99% identity with Bin2

sequences. Based on the sequence information provided herein, one of skill in the art can readily obtain full-length homologs and analogs.

As known in the art, "homology" or "identity" means the degree of sequence relatedness between two peptide or two nucleotide sequences as determined by the identity of the match between two lengths of such sequences. Both identity and homology can be readily calculated by methods extant in the prior art [See, e.g., COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, (1988); BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, (1993); COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, (1994); SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, (1987); and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, (1991)]. While there exist a number of methods to measure identity and homology between two nucleotide sequences, the terms "identity", "similarity" and homology are well known to skilled artisans [H. Carillo and D. Lipton, *SIAM J. Applied Math.*, 48:1073 (1988)]. Methods commonly employed to determine identity or homology between two sequences include, but are not limited to, those disclosed in GUIDE TO HUGE COMPUTERS, Martin J. Bishop, ed., Academic Press, San Diego, 1994. Preferred methods to determine identity or homology are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and homology between two sequences include, but are not limited to, the algorithm BESTFIT from the GCG program package [J. Devereux *et al.*, *Nucl. Acids Res.*, 12(1):387 (1984)], the related MACVECTOR program (Oxford), and the FASTA (Pearson) programs, which may be used at default settings or modified settings such as determined to be suitable by one of skill in the art.

A Bin2 peptide or protein of the present invention may also be modified to increase its ability to bind and thus, complex with, Bin1. For example, the Bin2 peptide or protein may be coupled to a chemical compounds or non-

proteinaceous carriers. In certain embodiments, the coupling is designed not to interfere with the desired biological activity of either the Bin2 peptide or protein or the carrier. For a review of some general considerations in coupling strategies, see Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, ed. E. Harlow and D. Lane (1988). For example, the carrier may be selected which facilitates cell penetration, e.g. a lipid or a carbohydrate. As another example, the carrier may be selected to deliver a toxin to Bin1, to which the Bin2 peptide binds. Such toxins are known to those of skill in the art and may include, e.g., chemical compounds including, without limitation, dinitrophenol groups and arsonic acid. Yet other carriers may be selected simply to facilitate production or delivery of the Bin2 peptide or protein. For example, useful carriers known in the art, include, without limitation, keyhole limpet hemocyanin (KLH); bovine serum albumin (BSA), ovalbumin, agarose beads; activated carbon; or bentonite.

The Bin2 peptides and proteins of the invention may also be modified by other techniques, such as by denaturation with heat and/or SDS. Alternatively, the peptides and proteins of the invention may be modified to provide an additional N- or C-terminal amino acid sequence suitable for biotinylation, e.g., cysteine or lysine.

B. Fragments/Deletion Mutants

Further encompassed by this invention are additional fragments of the Bin2 peptide or of the other proteins identified herein. Such fragments are desirably characterized by having a biological activity similar to that displayed by the complete protein, including, e.g., the ability to bind and complex with Bin1. These fragments may be designed or obtained in any desired length, including as small as about 5 to about 8 amino acids in length, about 14 or 15 amino acids in length, about 19 to 20 amino acids in length, or longer. Such a fragment represents less than the full-length Bin2 protein and may represent as little as a single epitope of the protein.

For example, one particularly desirable fragment of the invention is the BAR domain (amino acid 1 to 221 or amino acid 1 to 249 of SEQ ID NO:2), which contains dimerization signals. Optionally, one of skill in the art may utilize fragments with the BAR domain, which fragments are unique to BIN2, yet exhibit the desired

biological function. Suitably, fragments of the BAR domain are composed of at least 14 amino acids in length with respect to any fragment which encompasses all of amino acids 1 to 13 or which encompasses all of amino acids 23 to 35 or amino acids 23 to 45 of SEQ ID NO:2. Another desirable fragment encompasses the putative BAR
5 effector region (amino acid 138 to 155 of SEQ ID NO:2), which is implicated in Bin1 in tumor suppressor and programmed cell death signaling. Still other desirable fragments include fragments of about 8 or more amino acids from amino acids 250 to 564 of SEQ ID NO: 2, the C terminal region unrelated to other BAR family proteins. Suitably, any fragments of Bin2 containing these latter regions are at least 19 amino
10 acids in length.

In yet another example, a Bin2 fragment may be a T cell epitope. Such a T cell epitope may be readily identified may be readily identified using available computer modelling programs.

Optionally, the peptides of the invention may be modified to create
15 deletion mutants, for example, by truncation at the amino or carboxy termini, or by elimination of one or more amino acids. Still other modified fragments of Bin2 may be prepared by any number of now conventional techniques to improve production thereof, to enhance protein stability or other characteristics, e.g. binding activity or bioavailability, or to confer some other desired property upon the protein. Other
20 useful fragments of these polypeptides may be readily prepared by one of skill in the art using known techniques, such as deletion mutagenesis and expression.

C. *Fusion or Multimeric Proteins and Compositions*

The Bin2 peptides and protein of the present invention, or fragments of it, may also be constructed, using conventional genetic engineering techniques as part
25 of a larger and/or multimeric protein or protein compositions.

For example, such a fusion protein may be desirable in order to improve yield on expression and/or purification. Suitable fusion partners for such a purpose are well known to those of skill in the art and include, e.g., glutathione-S-transferase and maltose binding protein. Alternatively, a fusion protein of the

invention may be composed of a Bin2 fragment, such as a fragment corresponding to a T cell epitope or to the Bin1 binding region, which is fused to an active agent.

The active agent may be composed of other Bin2 peptides and proteins of this invention, or may be other proteinaceous materials or nucleic acid molecule.

- 5 For example, it may be desirable to fuse a Bin2 peptide or protein of the invention with a proteinaceous molecule which facilitates its cell penetration, e.g., *Drosophila antennapedia*, HIV Rev peptides, which are known to those of skill in the art. Alternatively, it may be desirable to fuse a Bin2 peptide or protein of the invention to a molecule which is to be targeted to a particular cell type and/or to Bin1. Particularly
- 10 suitable are toxins and anti-cancer agents, any of which are known to those of skill in the art. However, suitable examples include, without limitation, tetanus toxoid, cholera toxoid, PPD (purified protein derivative of tuberculin), and molecular toxins such as imidazole protein cross-linkers or other conjugates (which would kill a bound Bin1 molecule). These proteins are effective in the prevention, treatment and
- 15 diagnosis of cancers associated with inappropriate levels of functional Bin2 and/or inappropriate Bin1 function.

The fusion proteins of the invention are constructed for use in the methods and compositions of this invention. These fusion proteins may be produced recombinantly, or may be synthesized chemically.

- 20 A protein composition which may be a preferred alternative to the fusion proteins described above is a cocktail (i.e., a simple mixture) containing a Bin2 peptide or protein, or different mixtures of the Bin2 peptides and proteins of this invention. In still another aspect, the peptide and proteins of the invention may be provided with a detectable label, such as are described in detail below.

25 *D. Salts*

A peptide or protein antigen of the present invention may also be used in the form of a pharmaceutically acceptable salt. Suitable acids and bases which are capable of forming salts with the polypeptides of the present invention are well known to those of skill in the art, and include inorganic and organic acids and bases.

III. Methods of Making Proteins and Nucleic Acid Sequences of the
Invention Expression

The proteins and nucleic acid molecules of the invention may be isolated from natural sources as described above, or may be produced using chemical synthesis techniques, such as are well known to those of skill in the art. In still another alternative, the peptides and proteins of the invention may be produced using conventional chemical synthesis techniques, such as those described in G. Barony and R.B. Merrifield, *THE PEPTIDES: ANALYSIS, SYNTHESIS & BIOLOGY*, Academic Press, pp. 3-285 (1980), among others. Particularly desirable, is the use of recombinant technology to produce the proteins and nucleic acid sequences of the invention.

A. *Expression In Vitro*

To produce recombinant Bin2 proteins of this invention, a DNA sequence of the invention is inserted into a suitable expression system. Desirably, a recombinant molecule or vector is constructed in which the polynucleotide sequence encoding Bin2 is operably linked to a heterologous expression control sequence permitting expression of the Bin2 protein. Numerous types of appropriate expression vectors are known in the art for protein expression, by standard molecular biology techniques. Such vectors may be selected from among conventional vector types including insects, e.g., plasmids, yeast, fungal, bacterial, insect (e.g., baculovirus expression) or viral expression systems. Other appropriate expression vectors, of which numerous types are known in the art, can also be used for this purpose. Methods for obtaining such expression vectors are well-known. See, Sambrook et al, *MOLECULAR CLONING. A LABORATORY MANUAL*, 2d edition, Cold Spring Harbor Laboratory, New York (1989); Miller et al, *Genetic Engineering*, 8:277-298 (Plenum Press 1986) and references cited therein.

Suitable host cells or cell lines for transfection by this method include mammalian cells, such as human 293 cells, Chinese hamster ovary cells (CHO), the monkey COS-1 cell line or murine 3T3 cells derived from Swiss, Balb-c or NIH mice may be used. Another suitable mammalian cell line is the CV-1 cell line. Still other

suitable mammalian host cells, as well as methods for transfection, culture, amplification, screening, production, and purification are known in the art. [See, e.g., Gething and Sambrook, *Nature*, 293:620-625 (1981), or alternatively, Kaufman *et al*, *Mol. Cell. Biol.*, 5(7):1750-1759 (1985) or Howley *et al*, U. S. Patent 4,419,446].

5 Similarly bacterial cells are useful as host cells for the present invention. For example, the various strains of *E. coli* (e.g., HB101, MC1061, and strains used in the following examples) are well-known as host cells in the field of biotechnology. Various strains of *B. subtilis*, *Pseudomonas*, other bacilli and the like may also be employed in this method. Many strains of yeast cells known to those skilled in the art are also available as host cells for expression of the polypeptides of
10 the present invention. Other fungal cells may also be employed as expression systems. Alternatively, insect cells such as *Spodoptera frugiperda* (Sf9) cells may be used, e.g., in the baculovirus expression system.

Thus, the present invention provides a method for producing a
15 recombinant Bin2 protein which involves transfecting a host cell with at least one expression vector containing a recombinant polynucleotide encoding a Bin2 protein under the control of a transcriptional regulatory sequence, e.g., by conventional means such as electroporation. The transfected host cell is then cultured under conditions that allow expression of the Bin2 protein. The expressed protein is then recovered,
20 isolated, and optionally purified from the culture medium (or from the cell, if expressed intracellularly) by appropriate means known to one of skill in the art.

For example, the proteins may be isolated in soluble form following cell lysis, or may be extracted using known techniques, e.g., in guanidine chloride. If desired, the Bin2 proteins of the invention may be produced as a fusion protein. For
25 example, it may be desirable to produce Bin2 fusion proteins, to enhance expression of the protein in a selected host cell, to improve purification, or for use in monitoring the presence of Bin2 in cells, e.g., hepatocytes, or cell extracts. Suitable fusion partners for the Bin2 proteins of the invention are well known to those of skill in the art and include, among others, β -galactosidase, glutathione-S-transferase, and poly-histidine.
30

B. *Expression In Vivo*

Alternatively, where it is desired that the Bin2 protein be expressed *in vivo*, e.g., for therapeutic purposes, an appropriate vector for delivery of Bin2, or fragment thereof, may be readily selected by one of skill in the art. Exemplary vectors are readily available from a variety of academic and commercial sources, and include, e.g., DNA vectors (including "naked" DNA and plasmid systems), adeno-associated virus, adenovirus vectors, or other viral vectors, e.g., various poxviruses, vaccinia, etc. Methods for insertion of a desired gene, e.g. Bin2, and obtaining *in vivo* expression of the encoded protein, are well known to those of skill in the art.

IV. Antibodies Of the Invention

The Bin2 proteins of this invention are also useful as antigens for the development of anti-Bin2 antisera and antibodies to Bin2 or to a desired fragment of a Bin2 protein. Specific antisera may be generated using known techniques. See, Sambrook, cited above, Chapter 18, generally, incorporated by reference. Similarly, antibodies of the invention, both polyclonal and monoclonal, may be produced by conventional methods, including the Kohler and Milstein hybridoma technique and the many known modifications thereof. Similarly desirable antibodies are generated by applying known recombinant techniques to the monoclonal or polyclonal antibodies developed to these antigens [see, e.g., PCT Patent Application No. PCT/GB85/00392, British Patent Application Publication No. GB2188638A; Amit *et al.*, *Science*, 233:747-753 (1986); Queen *et al.*, *Proc. Nat'l. Acad. Sci. USA*, 86:10029-10033 (1989); PCT Patent Application No. PCT/WO9007861; and Riechmann *et al.*, *Nature*, 332:323-327 (1988); Huse *et al.*, *Science*, 246:1275-1281 (1988)], or any other techniques known to the art.

Given the disclosure contained herein, one of skill in the art may generate chimeric, humanized or fully human antibodies directed against a Bin2 peptide or protein of the invention by resort to known techniques by manipulating the complementarity determining regions of animals or human antibodies to the Bin2

protein of the invention. See, e.g., E. Mark and Padlin, "Humanization of Monoclonal Antibodies", Chapter 4, THE HANDBOOK OF EXPERIMENTAL PHARMACOLOGY, Vol. 113, The Pharmacology of Monoclonal Antibodies, Springer-Verlag (June, 1994).

5 Alternatively, the antigens may be assembled as multi-antigenic complexes [see, e.g., European Patent Application 0339695, published November 2, 1989] or as simple mixtures of antigenic proteins/peptides and employed to elicit high titer antibodies capable of binding the selected antigen(s) as it appears in the biological fluids of an infected animal or human.

10 Further provided by the present invention are anti-idiotypic antibodies (Ab2) and anti-anti-idiotypic antibodies (Ab3). Ab2 are specific for the target to which anti-Bin2 antibodies of the invention bind and Ab3 are similar to Bin2 antibodies (Ab1) in their binding specificities and biological activities [see, e.g., M. Wettendorff *et al.*, "Modulation of anti-tumor immunity by anti-idiotypic antibodies." In IDIOTYPIC
15 NETWORK AND DISEASES, ed. by J. Cerny and J. Hiernaux J, Am. Soc. Microbiol., Washington DC: pp. 203-229, (1990)]. These anti-idiotypic and anti-anti-idiotypic antibodies may be produced using techniques well known to those of skill in the art. Such anti-idiotypic antibodies (Ab2) can bear the internal image of the Bin1 and bind to it in much the same manner as Bin2 and are thus useful for the same
20 purposes as Bin2.

 In general, polyclonal antisera, monoclonal antibodies and other antibodies which bind to Bin2 as the antigen (Ab1) are useful to identify epitopes of Bin2, to separate Bin2 from contaminants in living tissue (e.g., in chromatographic columns and the like), and in general as research tools and as starting material essential for the
25 development of other types of antibodies described above. Anti-idiotypic antibodies (Ab2) are useful for binding Bin2 and thus may be used in the treatment of cancers in which Bin2 is part of a biochemical cascade of events leading to carcinoma. The Ab3 antibodies may be useful for the same reason the Ab1 are useful. Other uses as research tools and as components for separation of Bin2 from other contaminant of
30 living tissue, for example, are also contemplated for these antibodies.

For use in diagnostic assays, the antibodies are associated with conventional labels which are capable, alone or in concert with other compositions or compounds, of providing a detectable signal. Where more than one antibody is employed in a diagnostic method, the labels are desirably interactive to produce a detectable signal.

5 Most desirably, the label is detectable visually, e.g. colorimetrically. A variety of enzyme systems have been described in the art which will operate to reveal a colorimetric signal in an assay. As one example, peroxidase, which reacts with peroxide and a hydrogen donor such as tetramethyl benzidine (TMB), produces an oxidized TMB that is seen as a blue color. Other examples include horseradish

10 peroxidase (HRP) or alkaline phosphatase (AP), and hexokinase in conjunction with glucose-6-phosphate dehydrogenase which reacts with ATP, glucose, and NAD⁺ to yield, among other products, NADH that is detected as increased absorbance at 340 nm wavelength. Still another example is glucose oxidase (which uses glucose as a substrate) which releases peroxide as a product. Other label systems that may be

15 utilized in the methods of this invention are detectable by other means, e.g., colored latex microparticles [Bangs Laboratories, Indiana] in which a dye is embedded may be used in place of enzymes to form conjugates with the antibodies and provide a visual signal indicative of the presence of the resulting complex in applicable assays. Still other labels include fluorescent compounds, radioactive compounds or elements.

20 Detectable labels for attachment to antibodies useful in diagnostic assays of this invention may be easily selected from among numerous compositions known and readily available to one skilled in the art of diagnostic assays. The methods and antibodies of this invention are not limited by the particular detectable label or label system employed. Suitably, these detectable systems may also be utilized in

25 connection with diagnostic reagents composed of the peptides, proteins, and nucleic acid sequences of the invention.

V. Diagnostic Reagents and Methods

Advantageously, the present invention provides reagents and methods useful in detecting and diagnosing a deficiency in normal Bin2 levels and/or abnormal levels

of non-functional Bin2, and particularly deficiencies or excess production thereof, in a patient. Further, the present invention provides reagents which bind Bin1, and therefore as defined herein, a deficiency of Bin2 is an inadequate level of functional Bin2 to compensate for the levels of Bin1 in a patient. A deficiency of Bin1 is an
5 inadequate level of functional Bin1 to compensate for the levels of c-Myc in a patient. Conditions associated with deficiencies of Bin2 include hepatocarcinoma; conditions associated with Bin1 include a variety of cancers, e.g., epithelial cell cancer, breast cancer, melanoma, prostate cancer, liver cancer and colon cancer, and hyperplastic disease states, e.g., benign prostate hyperplasia. Conditions associated
10 with altered expression or loss of expression of normal Bin2 include myeloid and lymphoid leukemias.

For convenience, reference will be made to Bin2 proteins throughout this and the following section. However, it will be understood that Bin2 nucleic acids (including anti-sense sequences and oligonucleotide fragments, among others),
15 peptides, analogs and diagnostic compositions containing these molecules may be useful in these methods.

In one embodiment, this method involves detecting the presence of Bin1 (or other ligand for Bin2) which is produced by the affected human or animal patient's system and which are capable of binding to the Bin2 peptides and proteins (or Ab2)
20 of this invention or combinations thereof. This method comprises the steps of incubating a Bin2 peptide or protein of this invention with a sample of biological fluids from the patient. Bin1 present in the samples will form a complex with the Bin2 peptide or protein. Subsequently the reaction mixture is analyzed to determine the presence or absence of these complexes. The step of analyzing the reaction
25 mixture comprises contacting the reaction mixture with a labeled specific binding partner for the Bin2 ligand.

In one embodiment of the method, the Bin2 peptide or protein, or a mixture of the peptides and proteins of the invention is electro- or dot-blotted onto nitrocellulose paper. Subsequently, the biological fluid (e.g. serum or plasma) is incubated with the
30 blotted peptide or protein, and ligand (e.g., Bin1) in the biological fluid is allowed to

bind to the Bin2 peptide or protein. The bound ligand is then detected by standard immunoenzymatic methods.

In another embodiment of the method, latex beads are conjugated to the Bin2 peptide or protein of this invention. Subsequently, the biological fluid is incubated
5 with the bead/protein conjugate, thereby forming a reaction mixture. The reaction mixture is then analyzed to determine the presence of Bin1 or other Bin2 ligand.

In another embodiment, the diagnostic method of the invention involves detecting the presence of the naturally occurring Bin2 peptide or protein itself in its association with hepatocytes in the biological fluids of an animal or human infected
10 by the pathogen. This method includes the steps of incubating a ligand specific for Bin2 (e.g., Bin1 or an antibody of this invention, e.g. produced by administering to a suitable human and/or animal an antigen of this invention), preferably conventionally labelled for detection, with a sample of biological fluids from a human or an animal to be diagnosed. In the presence of Bin2, a complex is formed (specific binding
15 occurs). Subsequently, excess labeled antibody (or other ligand) is optionally removed, and the reaction mixture is analyzed to determine the presence or absence of the antigen-antibody complex and the amount of label associated therewith.

Assays employing a peptide or protein of the invention can be heterogenous (i.e., requiring a separation step) or homogenous. If the assay is heterogenous, a
20 variety of separation means can be employed, including centrifugation, filtration, chromatography, or magnetism.

One preferred assay for the screening of blood products or other physiological or biological fluids is an enzyme linked immunosorbant assay, i.e., an ELISA. Typically in an ELISA, the isolated Bin2 peptide or protein of the invention is
25 adsorbed to the surface of a microtiter well directly or through a capture matrix (i.e., antibody). Residual protein-binding sites on the surface are then blocked with an appropriate agent, such as bovine serum albumin (BSA), heat-inactivated normal goat serum (NGS), or BLOTTO (a buffered solution of nonfat dry milk which also contains a preservative, salts, and an antifoaming agent). The well is then incubated
30 with a biological sample suspected of containing Bin1 or another ligand specific for

Bin2. The sample can be applied neat, or more often, it can be diluted, usually in a buffered solution which contains a small amount (0.1-5.0% by weight) of protein, such as BSA, NGS, or BLOTTO. After incubating for a sufficient length of time to allow specific binding to occur, the well is washed to remove unbound protein and
5 then incubated with labeled anti-human immunoglobulin (α Hulg) or labeled antibodies to other species, e.g., dogs. The label can be chosen from a variety of enzymes, including horseradish peroxidase (HRP), β -galactosidase, alkaline phosphatase, and glucose oxidase, as described above. Sufficient time is allowed for specific binding to occur again, then the well is washed again to remove unbound
10 conjugate, and the substrate for the enzyme is added. Color is allowed to develop and the optical density of the contents of the well is determined visually or instrumentally.

Further, MAbs or other antibodies of this invention which are capable of binding to Bin2 peptides and proteins can be bound to ELISA plates. In another diagnostic method, the biological fluid is incubated on the antibody-bound plate and
15 washed. Detection of any antigen-antibody complex, and qualitative measurement of the labeled MAb is performed conventionally, as described above.

Other useful assay formats include the filter cup and dipstick. In the former assay, an antibody of this invention is fixed to a sintered glass filter to the opening of a small cap. The biological fluid or sample (5 mL) is worked through the filter. If
20 Bin1 is present, it will bind to the filter which is then visualized through a second Bin2 peptide or protein. The dipstick assay involves fixing an antigen or antibody to a filter, which is then dipped in the biological fluid, dried and screened with a detector molecule.

Other diagnostic assays can employ the antigen(s) or fragments of this
25 invention as nucleic acid probes or as anti-sense sequences, which can identify the presence of infection in the biological fluid by hybridizing to complementary sequences produced by the pathogen in the biological fluids. Such techniques, such as PCR, Northern or Southern hybridizations etc. are well known in the art.

It should be understood by one of skill in the art that any number of
30 conventional protein assay formats, particularly immunoassay formats, or nucleic

acid assay formats, may be designed to utilize the isolated antigens and antibodies or their nucleic acid sequences or anti-sense sequences of this invention for the detection of disorders associated with inappropriate/altered levels of functional Bin2 and/or for monitoring inappropriate levels of Bin1 in animals and humans. This invention is thus not limited by the selection of the particular assay format, and is believed to encompass assay formats which are known to those of skill in the art.

VI. Diagnostic Kits

For convenience, reagents for ELISA or other assays according to this invention may be provided in the form of kits. Such kits are useful for diagnosing conditions associated with dysfunctional Bin2 levels and/or Bin1 levels, including cancers in a human or an animal sample. Such a diagnostic kit contains an antigen of this invention and/or at least one antibody capable of binding an antigen of this invention, or the nucleic acid sequences encoding them, or their anti-sense sequences. Alternatively, such kits may contain a simple mixture of such antigens or sequences, or means for preparing a simple mixture.

These kits can include microtiter plates to which the Bin2 peptides, proteins, antibodies, or nucleic acid sequences of the invention have been pre-adsorbed, various diluents and buffers, labeled conjugates for the detection of specifically bound antigens or antibodies, or nucleic acids and other signal-generating reagents, such as enzyme substrates, cofactors and chromogens. Other components of these kits can easily be determined by one of skill in the art. Such components may include polyclonal or monoclonal capture antibodies, antigen of this invention, or a cocktail of two or more of the antibodies, purified or semi-purified extracts of these antigens as standards, MAb detector antibodies, an anti-mouse or anti-human antibody with indicator molecule conjugated thereto, an ELISA plate prepared for absorption, indicator charts for colorimetric comparisons, disposable gloves, decontamination instructions, applicator sticks or containers, and a sample preparator cup. Such kits provide a convenient, efficient way for a clinical laboratory to diagnose Bin2-associated conditions.

VII. Therapeutic Compositions and Methods

Compositions and methods useful for the treatment of conditions associated with inappropriate Bin2 levels are provided. Bin2 is expressed predominantly in blood, e.g., hematopoietic, cells and is upregulated during monocytic differentiation. Thus, Bin2 levels have been detected in spleen and peripheral blood leukocytes, and in thymus, colon and placenta, and Bin2 RNA has been strongly expressed in several human lymphoid and lymphoid cell lines, including GM1500, ALL200, BV173 and HL60. Bin2 was induced during granulocytic differentiation of HL60 cells, a promyelocytic leukemia cell line. Included among conditions related to Bin2 expression include disorders associated with blood cells and hepatocytes, including hepatocarcinomas and certain myeloid or lymphoid leukemias. Further, Bin2 may be useful in directing treatment to disorders associated with inappropriate Bin1 functions, and particularly, for inhibiting excessive Bin1 levels. These Bin1-associated disorders include liver, colorectal, prostate, and breast cancers, epithelial cell cancers, melanoma, and hyperplastic disease states.

The therapeutic compositions of the invention may be formulated to contain an anti-idiotypic antibody of the invention, the Bin2 protein itself or a fragment thereof, or nucleic acid sequences which direct expression of these antibodies, proteins or fragments thereof, including anti-sense sequences. The therapeutic composition desirably contains 0.01 μ g to 10 mg protein. These compositions may contain a pharmaceutically acceptable carrier, which facilitate administration of the compositions but are physiologically inert and/or nonharmful. Suitable carriers are well known to those of skill in the art and include, for example, saline. Alternatively, such compositions may include conventional delivery systems into which protein of the invention is incorporated. Optionally, these compositions may contain other active ingredients, e.g., chemotherapeutics.

Carriers may be selected by one of skill in the art. Exemplary carriers include sterile saline, lactose, sucrose, calcium phosphate, gelatin, dextran, agar, pectin, peanut oil, olive oil, sesame oil, and water. Additionally, the carrier or diluent may

include a time delay material, such as glycerol monostearate or glycerol distearate alone or with a wax. In addition, slow release polymer formulations can be used.

Optionally, this composition may also contain conventional pharmaceutical ingredients, such as preservatives, or chemical stabilizers. Suitable ingredients which
5 may be used in a therapeutic composition in conjunction with the antibodies include, for example, casamino acids, sucrose, gelatin, phenol red, N-Z amine, monopotassium diphosphate, lactose, lactalbumin hydrolysate, and dried milk.

Alternatively, or in addition to the antibodies of the invention, other agents useful in treating hepatocarcinoma or other conditions associated with dysfunctional
10 Bin2 levels, are expected to be useful in reducing or eliminating disease symptoms. Such agents may operate in concert with the therapeutic compositions of this invention. The development of therapeutic compositions containing these agents is within the skill of one in the art in view of the teachings of this invention.

According to the method of the invention, a human or an animal may be
15 treated for hepatocarcinoma by administering an effective amount of such a therapeutic composition. An "effective amount" may be between about 0.05 to about 1000 $\mu\text{g/mL}$ of a Bin2 peptide, protein or antibody of the invention. A suitable dosage may be about 1.0 mL of such an effective amount. Such a composition may be administered 1 - 3 times per day over a 1 day to 12 week period. However,
20 suitable dosage adjustments may be made by the attending physician or veterinarian depending upon the age, sex, weight and general health of the human or animal patient. Preferably, such a composition is administered parenterally, preferably intramuscularly or subcutaneously. However, it may also be formulated to be administered by any other suitable route, including orally or topically.

25 Still another composition contains Bin2 polynucleotide sequences which contain regulatory sequences which regulate expression of the proteins of the invention *in vivo* or *in vitro*. Generally, a DNA-based composition contains 0.05 μg to 1 mg DNA per mL dose. Where the antigen-encoding polynucleotide sequences are carried on a viral vector, a dose may be in the range of 1×10^3 pfu to 1×10^{13} pfu
30 per dose. However, the dose, timing and mode of administration of these

compositions may be determined by one of skill in the art. Such factors as the age, condition, and the level of the Bin2 deficiency detected by the diagnostic methods described above, may be taken into account in determining the dose, timing and mode of administration of the therapeutic compositions of the invention. Generally, where
5 treatment of an existing cancer or hyperplastic state is indicated, a therapeutic composition of the invention is preferably administered in a site-directed manner and is repeated as needed. Such therapy may be administered in conjunction with conventional therapies, including radiation and/or chemotherapeutic treatments.

VIII. Drug Screening and Development

10 The Bin2 peptides, antibodies and polynucleotide sequences of the present invention are also useful in the screening and development of chemical compounds or proteins which have utility as therapeutic drugs for the treatment of cancers associated with inappropriate Bin2 levels.

Suitable assay methods may be readily determined by one of skill in the art.
15 Where desired, and depending upon the assay selected, Bin2 may be immobilized directly or indirectly (e.g., via an anti-Bin2 antibody) on a suitable surface, e.g., in an ELISA format. Such immobilization surfaces are well known. For example, a wettable inert bead may be used. Alternatively, Bin2 may be used in screening assays which do not require immobilization, e.g., in the screening of combinatorial libraries.
20 Assays and techniques exist for the screening and development of drugs capable of binding to selected regions of Bin2. These include the use of a phage display system for expressing the Bin2 proteins, and using a culture of transfected *E. coli* or other microorganism to produce the proteins for binding studies of potential binding compounds. See, for example, the techniques described in G. Cesarini, FEBS
25 Letters, **307**(1):66-70 (July 1992); H. Gram *et al*, *J. Immunol. Meth.*, **161**:169-176 (1993); C. Summer *et al*, *Proc. Natl. Acad. Sci. USA*, **89**:3756-3760 (May 1992).

Other conventional drug screening techniques may be employed using the Bin2 peptides, antibodies or polynucleotides of this invention. As one example, a method for identifying compounds which specifically bind to a Bin2 protein can

include simply the steps of contacting a selected Bin2 protein with a test compound to permit binding of the test compound to the Bin2 protein; and determining the amount of test compound, if any, which is bound to the Bin2 protein. Such a method may involve the incubation of the test compound and the Bin2 protein immobilized on a solid support.

Typically, a surface containing the immobilized ligand is permitted to come into contact with a solution containing the Bin2 protein and binding is measured using an appropriate detection system. Suitable detection systems include, without limitation, the streptavidin horseradish peroxidase conjugate and direct conjugation by a tag, e.g. fluorescein. Other systems are well known to those of skill in the art. This invention is not limited by the detection system used.

Another method of identifying compounds which specifically bind to a Bin2 protein can include the steps of contacting a Bin2 protein immobilized on a solid support with both a test compound and the protein sequence which is a receptor for Bin2 to permit binding of the receptor to the Bin2 protein; and determining the amount of the receptor which is bound to the Bin2 protein. The inhibition of binding of the normal protein by the test compound thereby indicates binding of the test compound to the Bin2 protein.

In still another method, interaction blockers may be identified. As an example a simple plate assay could be used to screen for such blockers. In one embodiment of a plate assay one peptide/protein is bound to the dish and the other is added in an aqueous buffer (physiological KCl, e.g. 150 mM, and pH, eg. 7.5). Binding is monitored using an antibody to the peptide which is conjugated to a fluorescent or enzymological marker (e.g., fluorescein or HRP). The primary antibody could also be detected by using an anti-primary antibody that is so tagged. The binding conditions are empirically optimized for salt, pH, metal, and detergent conditions. Under optimized binding conditions, the assay is run in such a fashion that peptides or peptidomimetic drugs are added to the binding buffer. The positive control for blocking binding is provided by addition of excess Bin protein, whereas the negative control is an unrelated protein or scrambled peptide. For example, a

GST-Bin1 protein is used to coat a plate and a Bin2 peptide used for binding. The peptide is directly identified by an antibody; alternatively, it is epitope tagged. Still alternately, the peptide itself is conjugated to the marker desired. This type of assay is amenable to high throughput screening since it can be configured in a 96-well format.

Thus, through use of such methods, the present invention provides compounds capable of interacting with Bin2, or selected portions thereof, and either enhancing or inhibiting its biological activity, as desired. The assay methods described herein are also useful in screening for inhibition of Bin2. The solution containing the inhibitors may be obtained from any appropriate source, including, for example, extracts of supernatants from cultures of bioorganisms, extracts from organisms collected from natural sources, chemical compounds, and mixtures thereof.

The following examples illustrate the isolation and use of the Bin1 sequences of the invention. These examples are illustrative only and do not limit the scope of the invention.

EXAMPLE 1 - BIN2 IS A NOVEL BAR FAMILY ADAPTOR PROTEIN THAT LACKS AN SH3 DOMAIN

An anti-Bin1 polyclonal antisera was previously observed to crossreact with Bin1-related polypeptides in cells [Sakamuro *et al.*, *Nature Genet.* 14: 69-77 (1996)], suggesting that additional uncharacterized members of the BAR family existed in mammalian cells. Subsequent epitope mapping of the main regions of Bin1 recognized by this antisera defined a major epitope between the extreme C-terminus of the BAR domain [Wechsler-Reya *et al.*, *Cancer Res.* 57: 3258-3263 (1997)]. A TBLASTN search of the expressed sequence tag (EST) database with the amino acid sequence containing this epitope identified a germinal B cell cDNA (Genbank accession number AA452680) which encoded a polypeptide related to but nonidentical to amphiphysin or Bin1. Using this EST cDNA as a probe a full-length cDNA was obtained from a human leukocyte phage library and its complete DNA

sequence was determined using standard methods [see, e.g., Sambrook *et al.*, cited above]. A long open reading frame (ORF) identified in this cDNA encoded a 564 amino acid polypeptide rich in serine and glutamic acid with a predicted molecular weight of 61,709 Da (see Figs. 1A-1C). Using the BLAST2 algorithm to compare

5 Bin1 with this polypeptide, termed Bin2 (Bridging INtegrator-2), the presence of a complete BAR motif that had 61% identity and 75% similarity with boundaries of amino acid 1-249 of Bin2 and amino acid 1-251 of Bin1 (see Fig. 2) was confirmed. In particular, Bin2 was identical to Bin1 within a region of the latter (amino acid 138-155) which is most highly conserved region in BAR family proteins in evolution

10 (G.C.P., unpublished observations), whereas amphiphysin has a nonidentical residue in this region and was slightly less similar overall (data not shown). Bin2 lacked any canonical motifs other than the BAR domain (see Fig. 3). In particular, it lacked an SH3 domain which is found at the C-terminus of Bin1, amphiphysin, and RVS167. While RVS161 also lacks an SH3 domain, Bin2 differs in that it includes a large C-

15 terminus that extends beyond the BAR domain. Notably, Bin2 lacked sequences implicated in nonneuronal isoforms of Bin1 in interaction with c-Myc or TATA-binding protein in the nucleus [Sakamuro *et al.*, cited above] or in alternately spliced neuronal isoforms in interaction with clathrin [Ramjaun and McPherson, *J. Neurochem.* 70: 2369-2376 (1998)] or AP-2 (P. de Camilli, pers. comm.). Thus, the

20 structure of Bin2 suggested strongly that it represented a nonredundant function. Southern analysis confirmed the presence of Bin2 sequences in human genomic DNA (see below). It was concluded that Bin2 was a novel mammalian member of the BAR family of adaptor proteins.

25 EXAMPLE 2 - THE HUMAN BIN2 GENE IS LOCATED ON CHROMOSOME 4q22.1 AND EXHIBITS ABERRANT ORGANIZATION IN HEPATOMA CELLS

The Bin2 cDNA was used to isolate three human Bin2 genomic BAC clones by standard methods. Restriction analysis and Southern hybridization of these clones and comparison to genomic Southern hybridizations confirmed the presence of Bin2 sequences and ruled out the possibility that a pseudogene was cloned. One of the

clones, F727, was used to perform fluorescence *in situ* hybridization (FISH) analysis of metaphase chromosomes isolated from normal peripheral blood lymphocytes, essentially as described in *Cells: A Laboratory Manual*, vol. 3, p. 111.1-111.44, D. L. Spector et al, eds., Cold Spring Harbor Press, Cold Spring Harbor NY 1998.

5 More particularly, fluorescence *in situ* hybridization (FISH) was performed using a Bin2 genomic BAC clone labeled by nick translation with digoxigenin dUTP and metaphase chromosomes isolated from PHA-stimulated normal peripheral blood lymphocytes. A biotin-labelled probe specific for the centromere of chromosome 4 was prepared and also included in the hybridization. Slides were developed using a
10 fluoresceinated anti-digoxigenin antibodies and Texas red avidin.

Specific hybridization signals were detected on the long arm of a group B chromosome consistent with chromosome 4 on the basis of size, morphology, and banding pattern. An experiment which included a second probe specific for the centromere sequences of chromosome 4 confirmed this interpretation. A total of 80
15 metaphase cells analyzed with 73 exhibiting specific labeling. Measurements of 10 specifically labeled chromosomes 4 demonstrated that the Bin2-specific hybridization signal was located at a position 27% the distance from the centromere to the telomere of chromosome arm 4q, an area corresponding to band 4q22.1. Two studies have reported this region to be deleted in >50% of breast carcinomas [Schwendel *et al.*, *Br.*
20 *J. Cancer* **78**: 806-811 (1998)], with an even higher frequency in tumors harboring BRCA1 mutations [Tirkkonen *et al.*, *Cancer Res.* **57**: 1222-1227 (1997)], and a third study has reported this region to be deleted in >75% of hepatocarcinomas [Yeh *et al.*, *Gastroenterology* **110**: 184-192 (1996)]. The structure of the Bin2 gene in normal human foreskin, HepG2 or HLF hepatoma cells, and DU145 prostate carcinoma cells
25 was compared by genomic Southern analysis to assess the possibility of structural alteration.

For the Southern analysis, genomic DNA isolated from human foreskin, HepG2 or HLF hepatoma cells, or DU145 prostate carcinoma cells (as a negative control) was analyzed by standard Southern analysis using the Bin2 cDNA as a
30 hybridization probe. Both HepG2 and HLF exhibited normal and aberrant banding

patterns relative to normal foreskin and DU145 cells, which showed the same pattern as foreskin, consistent with alteration of at least one allele of the Bin2 gene in certain liver tumors. Similar to DU145, genomic DNAs isolated from a panel of nonmalignant and malignant B lymphoid cell lines (Daudi, Raji, 380, GM1500, G97, BV173) also did not exhibit aberrant organization of the Bin2 gene. It was concluded that the Bin2 gene localized to chromosome 4q22.1 within a region that was altered in hepatocellular tumors.

EXAMPLE 3 - EVIDENCE OF SIMILARITY BETWEEN BIN2, BIN1, AND DAXX

In an effort to gain insight into the function of Bin2, the sequences in its central and C-terminal regions were compared to the DNA database using the BLAST algorithm. Searches conducted with sequences derived from the central region of Bin2, including a C-terminal part of the BAR domain, revealed a region (amino acid 179-336) that was similar to a functionally undefined central region of Daxx, an adaptor protein implicated in Jun kinase (JNK) signaling and interactions with the programmed cell death receptor CD95/Fas in the cytosol and the centromere-binding protein CENP-C in the nucleus [Chang *et al.*, *Science* **281**: 1860-1863 (1998); Pluta *et al.*, *J. Cell Sci.* **111**: 2029-2041 (1998); Yang *et al.*, *Cell* **89**: 1067-1076 (1997); Zhang *et al.*, *Nature* **392**: 296-300 (1998)]. The alignment included part of the BAR domain and Bin1 and amphiphysin could also be aligned with Daxx. Table I illustrates the similarity between central regions of Bin2 and Daxx. Amino acid sequences from the central region of Bin2 were used to query the DNA database for related sequences using the TBLASTN algorithm. This figure provides the selected hits and significance scores. The query sequence was amino acid 179-336 in Bin2 [SEQ ID NO: 2]. The score for the Daxx hit was more significant than the hit to the related yeast BAR protein RVS161 (underlined). See, also, Figs. 4A and 4B.

Table 1			
	Sequences producing significant alignments	Score (bits)	E Value
5	gi 1438562 gb U60884 MMU60884 <i>Mus musculus</i> SH3P9 mRNA, complete...	117	1e-25
	gi 550449 gb U07616 HSU07616 Human amphiphysin mRNA, complete cds.	113	1e-24
	gi 2199534 gb AF001383 AF001383 Homo sapiens amphiphysin II mRNA...	113	2e-24
10	gi 1710134 gb U68485 HSU68485 Human Box-dependent MYC-interacti...	111	7e-24
	gi 2323471 gb AF015956 AF015956 Homo sapiens Fas-binding protein...	41	0.009
	gi 976346 gb L32832 HUMZFHP Homo sapiens zinc finger homeodoma...	40	0.020
15	gi 2745970 gb U84003 HSTSBN5 Homo sapiens putative tumor suppr...	39	0.058
	gi 1122811 emb Z68217 CEF58G6 <i>Caenorhabditis elegans</i> cosmid F58...	38	0.076
	gi 4417 emb X63315 SCRVS161 <i>S. cerevisiae</i> RVS 161 gene	38	0.076
20	gi 4057 emb X57185 SCNSR1 Yeast NSR1 gene for nuclear localizat...	37	0.22
	gi 29860 emb X55039 HSCENPB Human hCENP-B gene for centromere a...	36	0.29

25 However, whereas the extent and significance of the alignments to Bin1 and amphiphysin were relatively lower, the E value computed by BLAST for the Bin2-Daxx alignment ranked it stronger than that the analogous alignment between Bin2 and the yeast BAR family member RVS161 (9e-3 versus 7.6e-2, respectively). The rank related in part to a shared glutamate-rich segment found in Bin2 and Daxx but
30 absent from other BAR family members. It was concluded that Bin2 and Daxx shared a similar region of structure within a central region of each polypeptide.

The database comparisons identified a region of similarity between the central domains of Bin2 and Daxx, a nucleocytoplasmic adaptor protein linked to cell survival decisions and chromosome function. The functional implications of this relationship are unclear. Daxx was initially identified through its ability to interact with the death domain of CD95/Fas, a member of the tumor necrosis factor (TNF) superfamily of cell surface death receptors. Initial investigations suggested a role for Daxx in death signaling by CD95/Fas [Yang *et al.* 1997, cited above], but more recent studies have suggested that while Daxx may have a role in JNK signaling by the receptor it is dispensable for death signaling [Chang *et al.*, *Science* **281**: 1860-1863 (1998); Chang *et al.*, *Proc. Natl. Acad. Sci. USA* **96**: 1252-1256 (1999)]. Another study identified Daxx through its ability to interact with CENP-C, a centromere-binding protein. While the meaning of this interaction is not yet known, consistent with some nuclear role Daxx has also been found to interact with the cancer-related protein Pml and to localize to the subnuclear domain ND10 where Pml can be found (G. Maul, pers. comm.). Interestingly, Pml and Bin1 have each been demonstrated to have a role in certain types of programmed cell death [Quignon *et al.* *Nat. Genet.* **20**: 259-265 (1998); Wang *et al.*, *Nat. Genet.* **20**: 266-272 (1998)]. Therefore, it is tempting to speculate that the relationship between Daxx and Bin2 may reflect some related connection to cell survival controls. This possibility would be consistent with the apparent role of RVS proteins in yeast survival, following stresses which result from nutrient starvation.

EXAMPLE 4 - BIN2 IS EXPRESSED PREDOMINANTLY IN HEMATOPOIETIC CELLS AND IS UPREGULATED DURING MONOCYTIC DIFFERENTIATION

Northern analyses of total RNAs isolated from human tissues and cell lines was performed using the Bin2 cDNA as a hybridization probe to investigate the range of expression of Bin2 and to compare it with amphiphysin and Bin1 expression. Prior to Northern analysis, cells were treated with DMSO or RA for 1, 3 or 5 days and RNA was isolated for Northern analysis with Bin2 cDNA. The human tissues

studied included heart, brain, placenta, lung, liver, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, testis, ovary, small intestine, colon, and peripheral blood leukocytes. The cell lines included: Raji, 380, 697, VM173, GM1500, ALL200, Daudi, HepG2, Caco-2, HCT116, LoVo, HBL100, ZR75-1, MCF7, BT20, SK-BR-3, 5 A549, HLF, DU145, LNCaP, PC3, U373, U87-MG, and NCH2. Also determined was the level of Bin2 induction during differentiation of HL60 promyelocytic leukemia cells to monocytes.

Northern hybridization of human tissue blots obtained from Clontech initially suggested a broad range of expression, similar to Bin1 and in contrast to amphiphysin 10 (results not shown). Two Bin2 messages were noted in most tissues, suggesting alternate splicing as occurs in Bin1 [Wechsler-Reya *et al.*, *J. Biol. Chem.* 272: 31453-31458 (1997)]. The highest levels of Bin2 message were seen in spleen, peripheral blood leukocytes, thymus, placenta, testis, colon, liver, and lung. The pattern of expression more resembled Bin1, which is ubiquitous but expressed at highest levels 15 in skeletal muscle, than amphiphysin, which is essentially specific to the central nervous system. However, additional experiments suggested that Bin2 might be preferentially expressed in hemopoietic cells and that the apparent pattern of ubiquitous expression reflected contamination of various tissues with hematopoietic cells, where Bin2 was expressed at high levels. For example, Bin2 message was 20 barely detectable or undetectable by Northern analysis in 21 human cell lines derived from a variety of tissues, including breast, lung, prostate, brain, connective tissue (fibroblast), liver, and colon, despite the detection of Bin2 in these tissues. In contrast, Bin2 message was strongly expressed in several lymphoid cell lines (GM1500, ALL200, BV173, Jurkat) and in myeloid cells (HL60) that are derived 25 from the hematopoietic lineage. Given that the Bin2 gene may be altered in the cell lines examined, which were immortalized or malignant, it was possible that the inability to detect expression was due to functional loss. The likelihood that Bin2 was predominantly expressed in hematopoietic cells was supported by "virtual" Northern analyses, performed by comparing Bin2 sequences to the EST database, 30 which provides information about the source of the cDNA. The majority of identical

ESTs identified in this manner had been cloned from cDNA libraries derived from germinal B lymphoid cells, fetal liver (which is rich in B lymphoid cells), and placenta (which is rich in myeloid cells), although kidney libraries were also represented. One cell line identified to be positive for Bin2 expression was HL60
5 promyelocytic leukemia cells, which can be induced to differentiate to monocytes by treatment with dimethyl sulfoxide (DMSO) or to granulocytes by treatment with retinoic acid (RA). To assess the possibility that Bin2 may function in differentiated myeloid cells, it was determined whether the level of Bin2 message was altered during HL60 differentiation down the monocytic or granulocytic pathways. Northern
10 analysis demonstrated that Bin2 levels were increased within 5 days of DMSO but not RA treatment. The level of Bin2 following induction was similar to that found in human U937 myeloid cells and higher than in Jurkat T lymphoid cells. The elevation of Bin2 during differentiation was reminiscent of a similar elevation of Bin1 which occurs during differentiation of skeletal myoblasts and certain other cells including
15 smooth muscle and keratinocytes [Mao *et al.*, *Genomics* 56: 51-58 (1999); Wechsler-Reya *et al.* *Mol. Cell. Biol.* 18: 566-575 (1998)]. It was concluded that Bin2 was expressed predominantly in hematopoietic cells and was likely to function in the myeloid lineage.

Bin2 is expressed predominantly in hemapoietic cells. This pattern of
20 expression contrasts with amphiphysin, which is largely restricted to the central nervous system, as well as with Bin1, which is highly expressed in muscle but otherwise ubiquitous. Induction of Bin2 message was documented in a model system for monocytic differentiation, in support of the notion that Bin2 is likely to have an important function(s) in the hematopoietic lineage. Whether the Bin2 gene has
25 important functions in other tissues is not yet clear. While expression was documented by Northern analysis in many normal tissues, these results could be ascribed to contamination of tissues with hemapoietic cells: while Bin2 message was abundant in lymphoid and myeloid cells, it was undetectable in most benign and malignant non-hemapoietic cell lines examined. It is conceivable that some of the
30 deficits seen may be due to losses in malignant settings, such as is the case with Bin1

[Sakamuro *et al.*, *Nature Genet.* 14: 69-77 (1996)]. Consistent with this possibility, the Bin2 gene is located at chromosome 4q22.1, a region frequently disrupted in hepatocarcinoma, and aberrant organization of the gene was observed in two liver tumor lines. Bin2 was not expressed in these lines but little effect of ectopic Bin2 on the proliferation of these cell lines *in vitro* was noted, so the significance of the aberrant gene organization and possible loss of expression remains unclear.

EXAMPLE 5 - BIN2 AND BIN1 FORM A STABLE COMPLEX THAT REQUIRES THE BAR DOMAIN

Stable complexes have been reported in yeast between RVS161 and RVS167 and in brain between amphiphysin and brain-specific splice isoforms of Bin1 [Navarro *et al.*, *Biochim. Biophys. Acta*, 1343: 187-192 (1997); Wigge *et al.*, *Mol. Biol. Cell* 8: 2003-2015 (1997)]. Since Bin1 is expressed in hematopoietic cells, whether Bin2 and Bin1 could also form a stable biochemical complex was investigated. For coimmunoprecipitation experiments, Bin1 was *in vitro* translated in the presence or absence of Bin2 and complex formation was assessed by SDS-PAGE and fluorography after immunoprecipitation with the Bin1 monoclonal antibody 99D [Wechsler-Reya *et al.*, *Cancer Res.* 57: 3258-3263 (1997)].

Bin2 and Bin1 were *in vitro* translated with empty vector or cotranslated with each other in the presence of 35S-methionine. Products were fractionated on SDS-PAGE gels and fluorographed or subjected to immunoprecipitation with the anti-Bin1 antibody 99D [Wechsler-Reya *et al.*, *cited above*] before fractionation. Bin2 migrated with an apparent MW ~82 kD, which is greater than the predicted MW ~61 kD, reminiscent of a similar aberrant mobility displayed by Bin1, which has an apparent MW ~68 kD and a predicted MW ~50 kD. Bin2 was not immunoprecipitated by 99D unless cotranslated with Bin1.

Using a set of deletion mutants ($\Delta 124-207$, $\Delta 1-122$, $\Delta 152-207$, $\Delta 143-148$) the BAR domain in Bin1 was demonstrated to be required for Bin2 interaction. Deletion of the C-terminal region of BAR decreased binding efficiency, whereas deletion of residues 143-148 within a loop region implicated in effector signaling and

representing the most highly conserved part of the BAR domain in Bin1 had no effect. Deletion of the N-terminal region of BAR (residues 1-122) eliminated binding completely, arguing that the N-terminus of Bin1 was crucial for interaction with Bin2. Other deletion mutants of Bin1 lacking the so-called Unique central region, the
5 Myc-binding domain, or the SH3 domain, interacted with Bin2 with the same efficiency as wild-type Bin1 (data not shown). It was concluded that Bin1 and Bin2 formed a BAR domain-dependent complex in cells.

Bin1 and Bin2 were shown to form a stable biochemical complex, in the manner of RVS161 and RVS167 in yeast or amphiphysin and neuronal splice
10 isoforms of Bin1 in mammalian cells [Navarro *et al.*, cited above (1997); Wigge *et al.*, cited above (1997)], and the association depended upon the integrity of the BAR domain. Bin2 did not affect the tumor suppressor properties of Bin1 that are manifested in HepG2 cells [Sakamuro *et al.*, *Nature Genet.* 14: 69-77 (1996)]. This may reflect different requirements for each activity, since Bin2 association rested on
15 an N-terminal BAR determinant whereas the tumor suppressor activity of Bin1 rests upon a C-terminal BAR determinant. Evidence that BAR domains encode unique activities and are not functionally equivalent is provided by domain swapping studies performed in yeast [Sivadon *et al.*, *FEBS Lett.* 417: 21-27 (1997)]. Thus, the BAR
20 domain of Bin2 may have unique features, perhaps related to Bin1 regulation rather than effector signaling. In future work, it will be important to determine the physiological functions of Bin2 and how they are manifested independently or in an integrated manner with the functions of Bin1.

EXAMPLE 6 - BIN2 LACKS IN VITRO GROWTH INHIBITORY PROPERTIES

Bin1 has tumor suppressor properties in certain malignant cells [Sakamuro *et al.* 1996, cited above], so whether Bin2 had any similar effects and/or whether it
25 could influence the growth inhibitory activity of Bin1 was investigated. HepG2 hepatoma cells lack endogenous Bin1 and Bin2 expression so they provided a useful background to perform these experiments. Another cell line which lacks Bin2 expression, A549 lung carcinoma cells, was also used in these experiments. Cells

were transfected with the same expression vector used above, which carries a neomycin resistance cassette, and stably transformed cells were selected in growth media containing G418.

A ~2-fold decrease in colony formation efficiency relative to empty vector was noted in HepG2 cells but not in A549 cells (see Fig. 5A). These observations suggested that Bin2 may be weakly growth inhibitory. To confirm this, HepG2 colonies were ring-cloned, expanded into cell lines, and examined for ectopic Bin2 expression by Northern analysis. For Northern analysis, total cytoplasmic RNA was isolated from colonies that were ring-cloned and expanded into cell lines. Northern analysis was performed using Bin2 cDNA as probe. Robust levels of Bin2 mRNA were detected in several independent cell lines which did not exhibit any signs of growth inhibition, confirming that accumulation of Bin message was compatible with HepG2 proliferation. To determine if Bin2 could relieve or augment growth suppression by Bin1, a similar set of colony formation experiments was performed in HepG2 except that untagged empty vector or Bin2 vector was cotransfected with a neomycin resistance gene-tagged Bin1 vector [Sakamuro *et al.* 1996, cited above]. The number of colonies which emerged using Bin2 vectors was similar to those produced with control vector, indicating that Bin2 did not affect the ability of Bin1 to suppress HepG2 cell growth (see Fig. 5B). It was concluded that Bin2 lacked the strong growth inhibitory properties in Hep G2 cells that are inherent to Bin1.

All above-noted references and priority document are incorporated herein by reference. Numerous modifications and variations of the present invention are included in the above-identified specification and are expected to be obvious to one of skill in the art. Such modifications and alterations to the compositions and processes of the present invention are believed to be encompassed in the scope of the claims appended hereto.

WHAT IS CLAIMED IS:

1. A Bin2 protein having the amino acid sequence of SEQ ID NO:2.
2. A Bin2 peptide or protein selected from the group consisting of:
 - (a) a fragment of Bin2 comprising at least 8 amino acids in length, wherein any of said fragments comprising the sequence of amino acids 23 to 35 of SEQ ID NO:2 comprise at least 14 amino acids in length; and any fragments comprising the sequence of amino acids 138 to 155 of SEQ ID NO:2 comprise at least 19 amino acids in length;
 - (b) an analog or homolog of SEQ ID NO:2;
 - (c) a fusion protein comprising the amino acid sequence of (a) or (b) and a fusion partner;
 - (d) a deletion protein comprising the amino acid sequence of SEQ ID NO:2 with one to twenty amino acids deleted therefrom.
3. The Bin2 peptide or protein according to claim 2, wherein the fragment of Bin2 has the sequence of amino acids 1 to 221 of SEQ ID NO:2 or comprises at least the sequence of amino acids 138 to 155 of SEQ ID NO:2.
4. The Bin2 peptide or protein according to claim 2, wherein the fragment of Bin2 is at least 8 amino acids in length and comprising a sequence of contiguous amino acids selected from the sequence of amino acids 1 to 13 of SEQ ID NO: 2.
5. The Bin2 peptide or protein according to claim 2, wherein the fusion partner is selected from the group consisting of glutathione-S-transferase, β -galactosidase, poly-histidine and maltose binding protein.

6. A Bin2 nucleic acid sequence encoding a protein according to claim 1 or a fragment thereof.
7. A nucleic acid sequence selected from the group consisting of:
- (a) a nucleic acid sequence which hybridizes to the sequence of claim 1 under stringent conditions;
 - (b) a nucleic acid sequence complementary to the sequence of claim 1; and
 - (c) an allelic variant of any of (a) through (b).
8. A nucleic acid sequence encoding a fusion protein according to claim 2 or claim 5.
9. A vector comprising a nucleic acid sequence according to claim 6 under the control of regulatory sequences which direct expression of the Bin2 protein.
10. A vector comprising a nucleic acid sequence according to claims 7 or 8 said sequence under the control of regulatory sequences.
11. A host cell transformed with a vector according to claim 9 or 10.
12. A diagnostic reagent comprising a nucleic acid sequence of any of claims 6, 7, or 8 and a detectable label which is associated with said sequence.
13. A method for diagnosing hepatocarcinoma, said method comprising the steps of amplifying the DNA in a sample from a patient suspected of having hepatocarcinoma using a nucleic acid sequence according to claims 6 or 7.
14. A diagnostic reagent comprising a protein according to claim 1 or claim 2 and a detectable label which is associated with said protein.

15. A method for specifically diagnosing cancers associated with inappropriate expression of Bin1 comprising the steps of:
- contacting a sample from a human or animal to be diagnosed with the Bin2 protein of claim 1 or 2, or the diagnostic reagent of claim 12, whereby in the presence of Bin1 in the sample, a complex is formed between Bin1 and the Bin2 protein or reagent, and
 - analyzing for the presence or quantity of said complex.
16. An isolated anti-Bin2 antibody which is specific for the protein of claim 1 or 2.
17. The anti-Bin2 antibody according to claim 16, isolated by immunizing said host with the protein of claim 1 or the protein of claim 2.
18. The anti-Bin2 antibody according to claim 16 which is selected from the group consisting of a chimeric antibody, a humanized antibody, a monoclonal antibody and a polyclonal antibody.
19. A diagnostic reagent comprising the anti-Bin2 antibody according to claim 18 and a detectable label.
20. A method of diagnosing cancer or hyperplastic disease characterized by inappropriate levels of functional Bin1 levels in a human or an animal, said method comprising the steps of:
- contacting a Bin2 protein according to claim 1 or 2 or diagnostic reagent of claim 19 with a sample from a human or animal to be diagnosed, whereby in the presence of Bin1, a detectable complex is formed with the Bin2 protein or diagnostic reagent,

analyzing for the presence or absence of said complex; and
comparing the level of complex to a standard, wherein the absence of
said detectable label indicates the absence of or decreased levels of functional Bin1.

21. A kit for diagnosing a condition associated with Bin2 comprising a diagnostic reagent according to claims 19.
22. A composition comprising an effective amount of a Bin2 protein of claim 1 or claim 2 and a pharmaceutically acceptable carrier.
23. A method of detecting inappropriate expression of Box-dependent myc-interacting protein-2 (Bin2) in a patient comprising providing a sample from a patient suspected of having said inappropriate expression; incubating said sample in the presence of a diagnostic reagent according to claim 19; and comparing levels of expression to a normal Bin2 control.
24. A method of detecting inappropriate expression of Box-dependent myc-interacting peptide-2 (Bin 2) in a patient comprising providing a sample from a patient suspected of having said overexpression and performing nucleic acid amplification using the nucleic acid sequence according to claim 6 or claim 7.
25. A method of identifying compounds which specifically bind to Bin2, comprising the steps of contacting said Bin2 or a fragment thereof with a test compound to permit binding of the test compound to Bin2; and determining the amount of test compound which is bound to Bin2.

26. A method of identifying compounds which inhibit the binding of Bin2, comprising the steps of:

(a) contacting an amount of immobilized first Bin peptide or a fragment thereof with a test compound and an amount of labeled second Bin peptide or fragment, wherein said first Bin peptide is either a Bin1 or a Bin2 peptide, and the second Bin peptide is the Bin peptide that binds said first Bin peptide;

(b) separating unbound material from immobilized material of (a),
and

(c) measuring the amount of label on said immobilized material,
wherein a decrease in the amount of label immobilized in the presence of test compound compared to the amount of label immobilized in the presence of a control peptide or protein, indicates that said test compound inhibits the binding of Bin1 to Bin 2.

27. A compound identified by the method of claim 25 or 26.

ABSTRACT OF THE DISCLOSURE

The present invention provides Bin2 sequences and proteins encoded thereby. Also provided are compositions and methods utilizing these sequences and proteins in the diagnosis and treatment of blood disorders, including hepatocarcinoma. Further provided are oligonucleotides derived from sequences encoding Bin2, as well as compositions and methods utilizing same for diagnostic and therapeutic purposes.

5

FIGURE 1A

gcggccgcgt cgacgggagtg tggcagg atg gca gag ggc aag gca ggc ggc gcg 54
Met Ala Glu Gly Lys Ala Gly Gly Ala
1 5

gcc ggc ctc ttc gcc aag cag gtg cag aag aag ttt agc agg gcc cag 102
Ala Gly Leu Phe Ala Lys Gln Val Gln Lys Phe Ser Arg Ala Gln
10 15 20 25

gag aag gtg ctg cag aaa ttg ggg aaa gct gta gaa acc aaa gat gaa 150
Glu Lys Val Leu Gln Lys Leu Gly Lys Ala Val Glu Thr Lys Asp Glu
30 35 40

cga ttt gaa caa agc gct agc aac ttc tac caa caa cag gca gaa ggc 198
Arg Phe Glu Gln Ser Ala Ser Asn Phe Tyr Gln Gln Gln Ala Glu Gly
45 50 55

cac aag ctg tac aag gac ctg aag aac ttc ctt agt gca gtc aaa gtg 246
His Lys Leu Tyr Lys Asp Leu Lys Asn Phe Leu Ser Ala Val Lys Val
60 65 70

atg cat gaa agt tca aaa aga gtg tca gaa acc ctg cag gag atc tac 294
Met His Glu Ser Ser Lys Arg Val Ser Glu Thr Leu Gln Glu Ile Tyr
75 80 85

agc agc gag tgg gac ggt cat gag gag ctg aag gcc atc gta tgg aat 342
Ser Ser Glu Trp Asp Gly His Glu Glu Leu Lys Ala Ile Val Trp Asn
90 95 100 105

aat gat ctc ctt tgg gaa gac tac gag gag aaa ctg gct gac cag gct 390
Asn Asp Leu Leu Trp Glu Asp Tyr Glu Glu Lys Leu Ala Asp Gln Ala
110 115 120

gta agg acc atg gaa atc tat gtt gcc cag ttc agt gaa att aag gag 438
Val Arg Thr Met Glu Ile Tyr Val Ala Gln Phe Ser Glu Ile Lys Glu
125 130 135

aga att gcc aag cgg ggt cgg aaa ctc gtg gac tat gac agt gcc cga 486
Arg Ile Ala Lys Arg Gly Arg Lys Leu Val Asp Tyr Asp Ser Ala Arg
140 145 150

cac cac ctg gag gca gtg cag aat gcc aag aaa gat gag gcc aag act 534
His His Leu Glu Ala Val Gln Asn Ala Lys Lys Asp Glu Ala Lys Thr
155 160 165

gcc aag gca gag gaa gag ttc aac aaa gcc cag act gtg ttt gaa gat 582
Ala Lys Ala Glu Glu Glu Phe Asn Lys Ala Gln Thr Val Phe Glu Asp
170 175 180 185

ctg aac caa gaa cta cta gag gag ctg cct att ctt tat aat agt cgt 630
Leu Asn Gln Glu Leu Leu Glu Glu Leu Pro Ile Leu Tyr Asn Ser Arg
190 195 200

att ggc tgc tat gtg acc atc ttc caa aac att tcc aac ttg agg gat 678
Ile Gly Cys Tyr Val Thr Ile Phe Gln Asn Ile Ser Asn Leu Arg Asp
205 210 215

FIGURE 1B

gtc ttc tac agg gaa atg agc aag ctg aac cac aat ctc tac gag gtg	726
Val Phe Tyr Arg Glu Met Ser Lys Leu Asn His Asn Leu Tyr Glu Val	
220 225 230	
atg agc aaa ctg gag aag caa cat tcc aat aaa gtc ttt gtg gtg aag	774
Met Ser Lys Leu Glu Lys Gln His Ser Asn Lys Val Phe Val Val Lys	
235 240 245	
gga ctg tca agc agc agc agg cgc tct tta gtc att tct ccc cca gtt	822
Gly Leu Ser Ser Ser Arg Arg Ser Leu Val Ile Ser Pro Pro Val	
250 255 260 265	
cga aca gct aca gtc tcc agt cct ctt acc tca cct act agt ccc tct	870
Arg Thr Ala Thr Val Ser Ser Pro Leu Thr Ser Pro Thr Ser Pro Ser	
270 275 280	
aca ctt tcc ttg aag agt gag agt gaa tct gtc tca gca act gaa gat	918
Thr Leu Ser Leu Lys Ser Glu Ser Glu Ser Val Ser Ala Thr Glu Asp	
285 290 295	
ctg gca cct gat gca gcc caa ggg gaa gac aat tct gag atc aag gag	966
Leu Ala Pro Asp Ala Ala Gln Gly Glu Asp Asn Ser Glu Ile Lys Glu	
300 305 310	
ctc tta gaa gag gag gaa ata gag aag gaa gga tct gaa gca agc tcc	1014
Leu Leu Glu Glu Glu Glu Ile Glu Lys Glu Gly Ser Glu Ala Ser Ser	
315 320 325	
tct gag gaa gat gac cct cta cca gcc tgc aat ggc ccc gcc cag gcc	1062
Ser Glu Glu Asp Asp Pro Leu Pro Ala Cys Asn Gly Pro Ala Gln Ala	
330 335 340 345	
cag ccc tct cct acc act gag agg gcc aag tcc cag gag gaa gtt ctc	1110
Gln Pro Ser Pro Thr Thr Glu Arg Ala Lys Ser Gln Glu Glu Val Leu	
350 355 360	
ccc agc tcc aca act cca tca cca ggc gga gcc ctg agc cct tca ggg	1158
Pro Ser Ser Thr Thr Pro Ser Pro Gly Gly Ala Leu Ser Pro Ser Gly	
365 370 375	
cag cct tca tca tct gcc aca gaa gta gtc ctc cga acc cgc acc gca	1206
Gln Pro Ser Ser Ser Ala Thr Glu Val Val Leu Arg Thr Arg Thr Ala	
380 385 390	
agt gaa gga tct gaa caa cca aag aag aga gcc tct atc cag agg acc	1254
Ser Glu Gly Ser Glu Gln Pro Lys Lys Arg Ala Ser Ile Gln Arg Thr	
395 400 405	
tca gca ccc cct agt agg cct cct cca ccc aga gcc act gca agc ccc	1302
Ser Ala Pro Pro Ser Arg Arg Pro Pro Pro Arg Ala Thr Ala Ser Pro	
410 415 420 425	

FIGURE 1C

agg ccc tcc tca ggg aac ata cct tcc agc cct aca gcc tct gga ggg	1350
Arg Pro Ser Ser Gly Asn Ile Pro Ser Ser Pro Thr Ala Ser Gly Gly	
430 435 440	
ggt tca ccc acc agc cct agg gcc tcc ttg ggg act ggg act gca agt	1398
Gly Ser Pro Thr Ser Pro Arg Ala Ser Leu Gly Thr Gly Thr Ala Ser	
445 450 455	
cct agg acc tcc cta gag gtc tct cct aat cca gaa cca cca gag aag	1446
Pro Arg Thr Ser Leu Glu Val Ser Pro Asn Pro Glu Pro Pro Glu Lys	
460 465 470	
cca gta aga act cct gag gcc aaa gaa aat gaa aac atc cac aat cag	1494
Pro Val Arg Thr Pro Glu Ala Lys Glu Asn Glu Asn Ile His Asn Gln	
475 480 485	
aac cct gaa gaa ctt tgt act tcc ccc acc tta atg aca tct cag gtt	1542
Asn Pro Glu Glu Leu Cys Thr Ser Pro Thr Leu Met Thr Ser Gln Val	
490 495 500 505	
gct tca gag cct gga gag gca aag aag atg gaa gac aag gaa aag gat	1590
Ala Ser Glu Pro Glu Glu Ala Lys Lys Met Glu Asp Lys Glu Lys Asp	
510 515 520	
aat aag ctt atc tca gct gac tcc tcg gag ggc caa gac cag ctt caa	1638
Asn Lys Leu Ile Ser Ala Asp Ser Ser Glu Gly Gln Asp Gln Leu Gln	
525 530 535	
gtc tcc atg gta cca gaa aac aac aac ctc aca gca cct gaa cct caa	1686
Val Ser Met Val Pro Glu Asn Asn Asn Leu Thr Ala Pro Glu Pro Gln	
540 545 550	
gaa gag gta tcc aca agt gaa aat cca caa ctc tgaagagaaa ctaccaagac	1739
Glu Glu Val Ser Thr Ser Glu Asn Pro Gln Leu	
555 560	
tcctcctgcc ccaaacctcg ccagagaagc tcttcaacca gaggggtatag gtcagagggg	1799
tataagagcc agcatccatc cctgggttct cagtaggaat gctggtgctg tctaaagacc	1859
tggcattaat ggaggcggag gaggagcctt acgggaggga tggaggggagg caggctgggg	1919
agaagagaac attagactca gggaatatltt aattctggtt tttagcattat tagaataaga	1979
ctttatacat taactaaagt ggagctttta tcaactataaa aagcaaaagt atntatagac	2039
acagacactt gcctatacag agacataacc acacacactc agaggatagt gaacaaatct	2099
gtctttgact tacgacccat ttgcaagac ttaaagccga aagaacacat tttcagattg	2159
ttaataaag tctgattctg actaaaaaaaa aaaaaaa	2196

FIG. 2

Bin 2:	MAE - GKAGGAAGLFAKQVQKKFSRAQEKVLQ	30
Bin 1:	MAEMGSGKGV T AGKIASNVQKKLTRAQEKVLQ	31
Bin2:	KL GKAVETKDERFEQSAS NFYQQQAEGHKLY	61
Bin1:	KL GKADETKDEQFEQCVQNFNKQLT EGTRLQ	62
Bin2:	KDLKNFLSAVKVMHESS KRVSETLQEI Y SSEW	93
Bin1:	KDLRTYLASVKAMHEASKKLNELQEVVEPDW	94
Bin2:	DGHEELKA IVWNNDLLWE DYEEKLA DQAVR	123
Bin1:	P GRDEANKIAE NNDLLWM DYHQLVDQALL	124
Bin2:	TMEI YVAQFSEIKE RIAKRGRKLV DYDSARHH	155
Bin1:	TMDT YLGQFPDIKS RIAKRGRKLV DYDSARHH	156
Bin2:	LEAVQNA - KKDEAKT AKAE EEE FNKAQTVFED	185
Bin1:	YESL QTAK KKDEAKI AKAE EEE LI KAQKV FEE	187
Bin 2:	L NQELL EELPI LY NSR I GCYVTI FQNISNLRD	227
Bin 1:	MNVDLQEELPS LWNSRVGFVNTFQS IAGLEE	226
Bin2:	VFYREMSKLNHNLYEVM SKLEKQHSNKVFVVGK	250
Bin1:	NFHKEMSKLNQNLNDVLVGLEKQHG SNTFTVKA	252

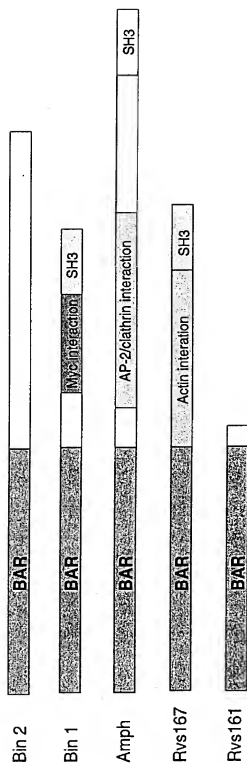
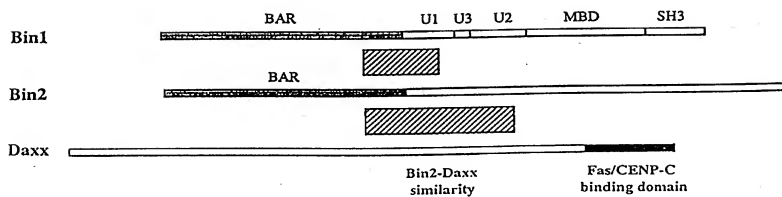


Fig. 3

Figure 4A

Bin1	AQK YFEENINVDLQEELP--SLVNSRYGYVNTFQSIAGLEENPHK-EMSKLNQNLNDVLVGLEKQHGSNTFTYKAQ.....U3-U2-NIED
	AQ VFG++N +L EELP L+ NSR+G YV FQ H+ L+ F++EMSKLN+NL +V+ LEKQH+ F VR
Bin2	AQTVEEDLNQELLEELP--ILYNSRIGCYVTFIQNISNLRDVFYR-EMSKLNHNLYEYMSKLEKQHSNKVVFVVKGLSSSSRSLSVISPPVRTATVS
	AQ F.D+ LE+ ++YN +GC++T +Y ++L N + +S+L++ S ++ G ++ R A
Daxx	AQDAFRDVGIRLQERRHLDLIYN--FCGCHLTDYRPGVDPALSYPSVARSRLRENRIALSRLDQVISFYAMLQDGGCEGKKK.....RRARLD
Bin	SPLTSPTSPTLSLKSSESVSATEDLAPDAAQGEDNSRKELL---EEEEIEKGESEASSSEDEPL
	P+ +P SL S + + P A+++E +E E EEEE E+E EA+ SEE+E L
Daxx	GISSHSANPPERSLDSGEGRIGMASQGCPSASRAETDDEDEESDEEEEEEEEEEEGATDSEEEEDL

Figure 4B

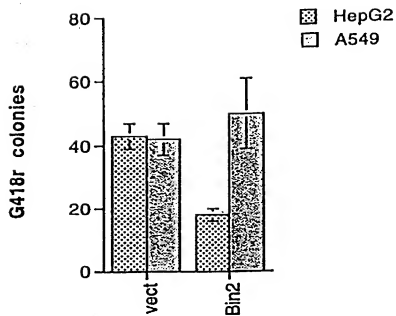


Figure 5A

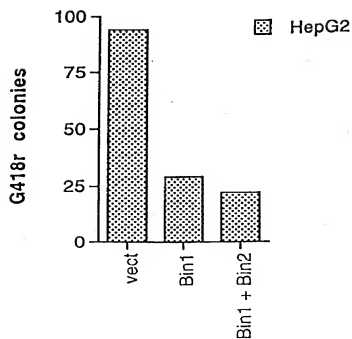


Figure 5B



00270

PATENT TRADEMARK OFFICE

**DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled BRIDGING INTEGRATOR-2 (BIN2) NUCLEIC ACID MOLECULES AND PROTEINS AND USES THEREFOR, the specification of which is attached hereto and was filed as PCT International Patent Application No. PCT/US00/23723, on August 30, 2000.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56, including for continuation-in-part applications, material information which became available between the filing date of the prior application and the national or PCT international filing date of the continuation-in-part application.

I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Priority
Not Claimed

Certified Copy
Attached?

(Number) (Country) (MM/DD/YYYY)

Yes

No

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States provisional application(s) listed below.

60/151,554
(Application Number)

August 31, 1999
(Filing Date, MM/DD/YYYY)

7
I hereby appoint the following attorneys and agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: STANLEY B. KITA, Registration No. 24,561; GEORGE A. SMITH, JR., Registration No. 34,442; MARY E. BAK, Registration No. 31,215; CATHY A. KODROFF, Registration Number 33,980; WILLIAM BAK, Registration Number 37,277; HENRY HANSEN, Registration No. 19,612; and TRACY U. PALOVICH, Registration No. 47,840.

Address all telephone calls to Mary E. Bak at telephone no. (215) 540-9206. Address all correspondence to HOWSON AND HOWSON, Spring House Corporate Center, P. O. Box 457, Spring House, Pennsylvania 19477.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

160 Full name of first inventor: George C. Prendergast

Inventor's signature [Signature] 1/18/02
Date

Residence: Bala Cynwyd, Pennsylvania 19004 PA

Citizenship: United States of America

Post Office Address: 414 Bryn Mawr Avenue, Bala Cynwyd, Pennsylvania 19004

Full name of second inventor: Kai Ge

Inventor's signature _____ Date _____

Residence: Philadelphia, Pennsylvania 19104

Citizenship: China

Post Office Address: 4427 Spruce Street, Philadelphia, Pennsylvania 19104

7
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Full name of first inventor: George C. Prendergast

Inventor's signature _____ Date _____

Residence: Bala Cynwyd, Pennsylvania 19004

Citizenship: United States of America

Post Office Address: 414 Bryn Mawr Avenue, Bala Cynwyd, Pennsylvania 19004

200
Full name of second inventor: Kai Ge

Inventor's signature Kai Ge Date Jan 17, 2002

Residence: Philadelphia, Pennsylvania 19104 PA

Citizenship: China

Post Office Address: 4427 Spruce Street, Philadelphia, Pennsylvania 19104

SEQUENCE LISTING

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Kai, Ge

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gta agg acc atg gaa atc tat gtt gcc cag ttc agt gaa att aag gag Val Arg Thr 125 Glu Ile Tyr Val Ala Gln Phe Ser Glu Ile Lys Glu 130 135			438
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Pro Gly	Gly Ala	Leu Ser	Pro Ser	Gly Gln	Pro Ser	Ser Ala
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Pro Pro	Pro Arg	Ala Thr	Ala Ser	Pro Arg	Pro Ser	Ser Gly
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Ala Ser	Leu Gly	Thr Gly	Thr Ala	Ser Pro	Arg Thr	Ser Leu
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Ser Pro	Asn Pro	Glu Pro	Pro Glu	Lys Pro	Val Arg	Thr Pro
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Lys Glu	Asn Glu	Asn Ile	His Asn	Gln Asn	Pro Glu	Glu Leu
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Ser Pro	Thr Leu	Met Thr	Ser Gln	Val Ala	Ser Glu	Pro Gly
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						510
Lys Lys	Met Glu	Asp Lys	Glu Lys	Asp Asn	Lys Leu	Ile Ser
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Ser Ser	Glu Gly	Gln Asp	Gln Leu	Gln Val	Ser Met	Val Pro
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Leu Arg Glu Asn Arg Ile Leu Ala Leu Ser Arg Leu Asp Gln Val Ile
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Ser Phe Tyr Ala Met Leu Gln Asp Gly Gly Glu Glu Gly Lys Lys Lys
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Lys Arg Arg Ala Arg Leu Asp
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